

SEQUENCE LISTING

<110> Helentjaris, Tim
Bates, Nic
Allen, Stephen M.

<120> Novel Invertase Inhibitors and Methods
of Use

<130> 035718/208677

<150> US 60/181,509

<151> 2000-02-10

<160> 54

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 665

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (68)...(598)

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Met Lys Leu Leu Gln Ala Leu Cys Pro Leu Val Ile Leu Leu	
1 5 10	
gcc tgc tcc acg tcc aac gct tcc gtc cta caa gac gcg tgc aag tcc	157
Ala Cys Ser Thr Ser Asn Ala Ser Val Leu Gln Asp Ala Cys Lys Ser	
15 20 25 30	
ttc gcc gct aag atc ccg gac acc ggc tac gcc tac tgc atc aag ttc	205
Phe Ala Ala Lys Ile Pro Asp Thr Gly Tyr Ala Tyr Cys Ile Lys Phe	
35 40 45	
ttc cag gcc gac agg gga agc gcc ggc gcg gac aag cgt ggc ctc gcc	253
Phe Gln Ala Asp Arg Gly Ser Ala Gly Ala Asp Lys Arg Gly Leu Ala	
50 55 60	
gcc atc gcc gtg agg atc atg ggg gca gcc gcc aag agc acc gcc agt	301
Ala Ile Ala Val Arg Ile Met Gly Ala Ala Ala Lys Ser Thr Ala Ser	
65 70 75	
cac atc gcc gcc ctg cgg gcc tcc gag aag gac aag gag cgg ctg gcg	349
His Ile Ala Ala Leu Arg Ala Ser Glu Lys Asp Lys Glu Arg Leu Ala	
80 85 90	

tgc	ctc	agc	gat	tgc	tcc	gag	gtg	tac	gcg	cag	gcc	gtg	gac	cag	acc	397
Cys	Leu	Ser	Asp	Cys	Ser	Glu	Val	Tyr	Ala	Gln	Ala	Val	Asp	Gln	Thr	
95					100					105					110	

ggc	gtg	gcg	gcg	aag	ggc	atc	gcc	tcg	ggc	acg	ccc	cgg	ggc	cgc	gcg	445
Gly	Val	Ala	Ala	Lys	Gly	Ile	Ala	Ser	Gly	Thr	Pro	Arg	Gly	Arg	Ala	
				115					120					125		

gac	gcg	gtg	atg	gcg	ctc	agc	acg	gtg	gag	gat	gcc	ccc	ggc	acc	tgt	493
Asp	Ala	Val	Met	Ala	Leu	Ser	Thr	Val	Glu	Asp	Ala	Pro	Gly	Thr	Cys	
			130					135					140			

gag	cag	ggg	ttc	cag	gac	ctg	agc	gtg	cgt	tcg	ccg	ctg	gcc	tcg	gag	541
Glu	Gln	Gly	Phe	Gln	Asp	Leu	Ser	Val	Arg	Ser	Pro	Leu	Ala	Ser	Glu	
		145				150						155				

gac	gcc	ggg	ttc	cgg	aag	gat	gcg	tcc	atc	gcg	ctg	tct	gta	acg	gcc	589
Asp	Ala	Gly	Phe	Arg	Lys	Asp	Ala	Ser	Ile	Ala	Leu	Ser	Val	Thr	Ala	
	160				165					170						

gcg	ttg	taa	gcaaaggtgt	ataatccttt	tcgatatagg	ttaaaaatga	638
Ala	Leu	*					
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ataaaaaaaaa	aaaaaaaaagg	cgccgcg	665
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Ser	Thr	Ser	Asn	Ala	Ser	Val	Leu	Gln	Asp	Ala	Cys	Lys	Ser	Phe	Ala
			20					25				30			
Ala	Lys	Ile	Pro	Asp	Thr	Gly	Tyr	Ala	Tyr	Cys	Ile	Lys	Phe	Phe	Gln
		35				40					45				
Ala	Asp	Arg	Gly	Ser	Ala	Gly	Ala	Asp	Lys	Arg	Gly	Leu	Ala	Ala	Ile
	50				55					60					
Ala	Val	Arg	Ile	Met	Gly	Ala	Ala	Ala	Lys	Ser	Thr	Ala	Ser	His	Ile
65				70					75					80	
Ala	Ala	Leu	Arg	Ala	Ser	Glu	Lys	Asp	Lys	Glu	Arg	Leu	Ala	Cys	Leu
			85					90						95	
Ser	Asp	Cys	Ser	Glu	Val	Tyr	Ala	Gln	Ala	Val	Asp	Gln	Thr	Gly	Val
			100					105					110		
Ala	Ala	Lys	Gly	Ile	Ala	Ser	Gly	Thr	Pro	Arg	Gly	Arg	Ala	Asp	Ala
		115				120						125			
Val	Met	Ala	Leu	Ser	Thr	Val	Glu	Asp	Ala	Pro	Gly	Thr	Cys	Glu	Gln
	130					135					140				
Gly	Phe	Gln	Asp	Leu	Ser	Val	Arg	Ser	Pro	Leu	Ala	Ser	Glu	Asp	Ala
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Gly	Phe	Arg	Lys	Asp	Ala	Ser	Ile	Ala	Leu	Ser	Val	Thr	Ala	Ala	Leu

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 gcctactgca tcaagttctt ccaggccgac aggggaagcg ccggcgcgga caagcgtggc 180
 ctgcgcgcca tcgccgtgag gatcatgggg gcagccgcca agagcaccgc cagtcacatc 240
 gccgccctgc gggcctccga gaaggacaag gagcggctgg cgtgcctcag cgattgctcc 300
 gaggtgtacg cgcaggccgt ggaccagacc ggcgtggcgg cgaagggcat cgctcgggc 360
 acgccccggg gccgcgcgga cgcggtgatg gcgctcagca cggaggagga tgccccggc 420
 acctgtgagc aggggttcca ggacctgagc gtgcgttcgc cgctggcctc ggaggacgcc 480
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<220>
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 <222> (58) ... (723)

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gca acc acc aag agg gag aag gtc atc ctc gtc ctg ctg ttc tcc ctg 108
 Ala Thr Thr Lys Arg Glu Lys Val Ile Leu Val Leu Leu Phe Ser Leu
 5 10 15

acg atg ctc cct ctc agc acc ctc ggc acc cgc tcc ggc ccg gcg gcc 156
 Thr Met Leu Pro Leu Ser Thr Leu Gly Thr Arg Ser Gly Pro Ala Ala
 20 25 30

gtg cag cac cac ggc cac ggc ggc acc acc aag cac ccc tcg cct cct 204
 Val Gln His His Gly His Gly Gly Thr Thr Lys His Pro Ser Pro Pro
 35 40 45

tca cca gcc acg gcg gcg ctg gta cgc agc acg tgt aac tcc acg gcg 252
 Ser Pro Ala Thr Ala Ala Leu Val Arg Ser Thr Cys Asn Ser Thr Ala
 50 55 60 65

tac tac gac gtg tgc gtg tcc gcg ctg ggc gcc gac ccg tcc agc gcc 300
 Tyr Tyr Asp Val Cys Val Ser Ala Leu Gly Ala Asp Pro Ser Ser Ala
 70 75 80

acc gcc gac gtc cgc ggg ctc tcg acc atc gcc gtg tcc gcg gcg gcc 348

Thr	Ala	Asp	Val	Arg	Gly	Leu	Ser	Thr	Ile	Ala	Val	Ser	Ala	Ala	Ala		
			85					90					95				
gcc	aac	gcc	tcg	ggc	ggc	gcc	gcc	acg	gcc	gcg	gcg	ctc	gcc	aac	ggc		396
Ala	Asn	Ala	Ser	Gly	Gly	Ala	Ala	Thr	Ala	Ala	Ala	Leu	Ala	Asn	Gly		
		100					105					110					
acc	ggc	acc	gcg	tcg	tcg	tcc	aac	gcg	cag	gcg	gcc	cct	gcc	acg	gcc		444
Thr	Gly	Thr	Ala	Ser	Ser	Ser	Asn	Ala	Gln	Ala	Ala	Pro	Ala	Thr	Ala		
		115				120					125						
tcc	gcc	gcc	gcg	gcg	ctg	ctc	cgc	acg	tgc	gca	gcc	aag	tac	ggc	cag		492
Ser	Ala	Ala	Ala	Ala	Leu	Leu	Arg	Thr	Cys	Ala	Ala	Lys	Tyr	Gly	Gln		
		130			135					140					145		
gcc	cgg	gac	gcg	ctg	gcc	gcc	gcc	ggg	gac	tcc	atc	gcg	cag	cag	gac		540
Ala	Arg	Asp	Ala	Leu	Ala	Ala	Ala	Gly	Asp	Ser	Ile	Ala	Gln	Gln	Asp		
			150					155						160			
tac	gac	gtg	gcg	tcc	gtg	cac	gtg	agc	gcc	gcc	gcc	gag	tac	ccg	cag		588
Tyr	Asp	Val	Ala	Ser	Val	His	Val	Ser	Ala	Ala	Ala	Glu	Tyr	Pro	Gln		
		165					170						175				
gtg	tgt	agg	gtg	ctg	ttc	cgg	cgg	cag	aag	ccc	ggg	cag	tac	ccc	gcg		636
Val	Cys	Arg	Val	Leu	Phe	Arg	Arg	Gln	Lys	Pro	Gly	Gln	Tyr	Pro	Ala		
		180				185						190					
gag	ctg	gcg	gcg	agg	gag	gag	acg	ctc	agg	cag	ctc	tgc	tcc	gtc	gcg		684
Glu	Leu	Ala	Ala	Arg	Glu	Glu	Thr	Leu	Arg	Gln	Leu	Cys	Ser	Val	Ala		
		195				200				205							
ctc	gac	atc	atc	ggg	ctc	gcc	tcc	acc	aac	acc	aac	taa	taagctagca				733
Leu	Asp	Ile	Ile	Gly	Leu	Ala	Ser	Thr	Asn	Thr	Asn	*					
		210			215					220							
gcagtggcgt	ggcggcgaga	aaagagagga	agattaaaaa	aaagtagcac	ctttttcttt												793
ttggtttaat	tactgtacgt	attatatata	ttagcagggc	acatgcacgc	agatgcatat												853
ttaaattata	aaaagggttg	tgtgcctgcc	caatcaccgt	ttgaagaatt	atttgagcag												913
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aactcgag																	981

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 <213> Zea mays

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 Ala Val Gln His His Gly His Gly Gly Thr Thr Lys His Pro Ser Pro
 35 40 45

Pro Ser Pro Ala Thr Ala Ala Leu Val Arg Ser Thr Cys Asn Ser Thr
 50 55 60
 Ala Tyr Tyr Asp Val Cys Val Ser Ala Leu Gly Ala Asp Pro Ser Ser
 65 70 75 80
 Ala Thr Ala Asp Val Arg Gly Leu Ser Thr Ile Ala Val Ser Ala Ala
 85 90 95
 Ala Ala Asn Ala Ser Gly Gly Ala Ala Thr Ala Ala Ala Leu Ala Asn
 100 105 110
 Gly Thr Gly Thr Ala Ser Ser Ser Asn Ala Gln Ala Ala Pro Ala Thr
 115 120 125
 Ala Ser Ala Ala Ala Ala Leu Leu Arg Thr Cys Ala Ala Lys Tyr Gly
 130 135 140
 Gln Ala Arg Asp Ala Leu Ala Ala Ala Gly Asp Ser Ile Ala Gln Gln
 145 150 155 160
 Asp Tyr Asp Val Ala Ser Val His Val Ser Ala Ala Ala Glu Tyr Pro
 165 170 175
 Gln Val Cys Arg Val Leu Phe Arg Arg Gln Lys Pro Gly Gln Tyr Pro
 180 185 190
 Ala Glu Leu Ala Ala Arg Glu Glu Thr Leu Arg Gln Leu Cys Ser Val
 195 200 205
 Ala Leu Asp Ile Ile Gly Leu Ala Ser Thr Asn Thr Asn
 210 215 220

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 <212> DNA
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 ggcaccacca agcaccctc gcctccttca ccagccacgg cggcgctggt acgcagcacg 180
 tgtaactcca cggcgtaacta cgacgtgtgc gtgtccgcgc tgggcgccga cccgtccagc 240
 gccaccgccc acgtccgcgg gctctcgacc atcgccgtgt ccgcggcggc cgccaacgcc 300
 tcggggcggc ccgccacggc cgcggcgctc gccaacggca ccggcaccgc gtcgtcgtcc 360
 aacgcgcagg cggccctcgc cacggcctcc gccgcgcgg cgctgctccg cacgtgcgca 420
 gccaaagtac gccaggccc ggacgcgctg gccgccggc gggactccat cgcgcagcag 480
 gactacgacg tggcgctccgt gcacgtgagc gccgcgcgc agtaccgcga ggtgtgtagg 540
 gtgctgttcc ggcggcagaa gcccgggcag taccgcgcgg agctggcggc gagggaggag 600
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 <212> DNA
 <213> Vitis L

<220>
 <221> CDS
 <222> (6)...(644)

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1				5				10						15	
gca gct att gtt gct ctc ttc ttc ttc tac ctc tca ctc aca aca cca															98
Ala Ala Ile Val Ala Leu Phe Phe Phe Tyr Leu Ser Leu Thr Thr Pro															
			20					25						30	
tgc tcg gcg gcc tca cca gag ccc cat ccc cct acc aat act aca caa															146
Cys Ser Ala Ala Ser Pro Glu Pro His Pro Pro Thr Asn Thr Thr Gln															
			35				40						45		
ttc atc aga acc tca tgc gga gtg act atg tac cct aag cta tgc ttc															194
Phe Ile Arg Thr Ser Cys Gly Val Thr Met Tyr Pro Lys Leu Cys Phe															
			50				55						60		
aaa acc ctc tcg gct tat gcc agc acc atc caa aca agc cat atg gag															242
Lys Thr Leu Ser Ala Tyr Ala Ser Thr Ile Gln Thr Ser His Met Glu															
			65				70						75		
ttg gcc aat gca gcc ctc tgt gtg agc cta aag ggc gct caa tcc tct															290
Leu Ala Asn Ala Ala Leu Cys Val Ser Leu Lys Gly Ala Gln Ser Ser															
			80				85						90		95
tca aac aag gta ctg aag tta tca aaa ggg cag ggg cta agc cgt aga															338
Ser Asn Lys Val Leu Lys Leu Ser Lys Gly Gln Gly Leu Ser Arg Arg															
			100											110	
gaa gcc gca gcg ata acg gat tgc att gag aac atg cag gac tcg gtg															386
Glu Ala Ala Ala Ile Thr Asp Cys Ile Glu Asn Met Gln Asp Ser Val															
			115				120						125		
gat gag ctc caa caa tct ctg gtg gcg atg aag gac ctt caa ggg cct															434
Asp Glu Leu Gln Gln Ser Leu Val Ala Met Lys Asp Leu Gln Gly Pro															
			130				135						140		
gat ttt caa atg aaa atg agt gat ata gtg aca tgg gtg agt gca gct															482
Asp Phe Gln Met Lys Met Ser Asp Ile Val Thr Trp Val Ser Ala Ala															
			145				150						155		
ctg aca gat gaa gac aca tgc atg gat gga ttc gca gag cat gcc atg															530
Leu Thr Asp Glu Asp Thr Cys Met Asp Gly Phe Ala Glu His Ala Met															
			160				165						170		175
aaa ggg gac ctt aag agc act att agg agc aat att gtg agt gtt gct															578
Lys Gly Asp Leu Lys Ser Thr Ile Arg Ser Asn Ile Val Ser Val Ala															
			180											190	
cag tta acc agc aat gct ttg gcc atc atc aac aag ttt cta tct att															626
Gln Leu Thr Ser Asn Ala Leu Ala Ile Ile Asn Lys Phe Leu Ser Ile															
			195				200						205		
cag ggc aat caa ctc taa gttactgtgt cctatgtgtc tactactagt															674
Gln Gly Asn Gln Leu *															

210

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aaagaaatat ttgctaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 779

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<213> Vitis L

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Ser Ala Ala Ser Pro Glu Pro His Pro Pro Thr Asn Thr Thr Gln Phe
35 40 45
Ile Arg Thr Ser Cys Gly Val Thr Met Tyr Pro Lys Leu Cys Phe Lys
50 55 60
Thr Leu Ser Ala Tyr Ala Ser Thr Ile Gln Thr Ser His Met Glu Leu
65 70 75 80
Ala Asn Ala Ala Leu Cys Val Ser Leu Lys Gly Ala Gln Ser Ser Ser
85 90 95
Asn Lys Val Leu Lys Leu Ser Lys Gly Gln Gly Leu Ser Arg Arg Glu
100 105 110
Ala Ala Ala Ile Thr Asp Cys Ile Glu Asn Met Gln Asp Ser Val Asp
115 120 125
Glu Leu Gln Gln Ser Leu Val Ala Met Lys Asp Leu Gln Gly Pro Asp
130 135 140
Phe Gln Met Lys Met Ser Asp Ile Val Thr Trp Val Ser Ala Ala Leu
145 150 155 160
Thr Asp Glu Asp Thr Cys Met Asp Gly Phe Ala Glu His Ala Met Lys
165 170 175
Gly Asp Leu Lys Ser Thr Ile Arg Ser Asn Ile Val Ser Val Ala Gln
180 185 190
Leu Thr Ser Asn Ala Leu Ala Ile Ile Asn Lys Phe Leu Ser Ile Gln
195 200 205
Gly Asn Gln Leu
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<210> 9
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<212> DNA
<213> Vitis l

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ccccctacca atactacaca attcatcaga acctcatgcg gagtgactat gtaccctaag 180
ctatgcttca aaaccctctc ggcttatgcc agcaccatcc aaacaagcca tatggagtgt 240
gccaatgcag ccctctgtgt gagcctaaag ggcgctcaat cctcttcaaa caagggtactg 300
aagttatcaa aagggcaggg gctaagccgt agagaagccg cagcgataac ggattgcatt 360
gagaacatgc aggactcggg ggatgagctc caacaatctc tgggtggcgat gaaggacctt 420

caagggcctg attttcaaat gaaaatgagt gatatagtga catgggtgag tgcagctctg	480
acagatgaag acacatgcat ggatggattc gcagagcatg ccatgaaagg ggaccttaag	540
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<210> 10
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1 5 10 15	

ctc ctc ttc cat tct tgc ctt tcc tgt caa ctc atc cat caa aca tgc	98
Leu Leu Phe His Ser Ser Leu Ser Cys Gln Leu Ile His Gln Thr Cys	
20 25 30	

aag aga att gca gac aat gat ccc aat gtg agc tac aat tta tgc gtc	146
Lys Arg Ile Ala Asp Asn Asp Pro Asn Val Ser Tyr Asn Leu Cys Val	
35 40 45	

atg agc ctt gaa tca aat ccc atg agt gca aat gcg agc ctt gaa gaa	194
Met Ser Leu Glu Ser Asn Pro Met Ser Ala Asn Ala Ser Leu Glu Glu	
50 55 60	

ctt gga gtc atc gca gtc gag cta gcc ttg tct aat gcg aca tac atc	242
Leu Gly Val Ile Ala Val Glu Leu Ala Leu Ser Asn Ala Thr Tyr Ile	
65 70 75	

aat tgg tac att agc aat aag ctt ttg cag gag aaa ggg ttt gat cca	290
Asn Trp Tyr Ile Ser Asn Lys Leu Leu Gln Glu Lys Gly Phe Asp Pro	
80 85 90 95	

ttt gcc gag gct tgc cta aaa gat tgt cat gaa ctt tac tcc gac gcc	338
Phe Ala Glu Ala Cys Leu Lys Asp Cys His Glu Leu Tyr Ser Asp Ala	
100 105 110	

atc cct gag tta aaa gat gtg ctc gat gat ttt aag gac aaa gac tac	386
Ile Pro Glu Leu Lys Asp Val Leu Asp Asp Phe Lys Asp Lys Asp Tyr	
115 120 125	

tac aag gct aat ata gag ttg agc gca gcc atg gag gcg tgc gct act	434
Tyr Lys Ala Asn Ile Glu Leu Ser Ala Ala Met Glu Ala Ser Ala Thr	
130 135 140	

tgt gaa gat ggt tac aag gaa agg aaa ggt gaa gtg tct ccc ttg gca	482
Cys Glu Asp Gly Tyr Lys Glu Arg Lys Gly Glu Val Ser Pro Leu Ala	

145	150	155	
aaa gag gac aac aac ttc ttt caa ttg tgt gca att gct ctt gct ttc			530
Lys Glu Asp Asn Asn Phe Phe Gln Leu Cys Ala Ile Ala Leu Ala Phe			
160	165	170	175

act aat atg ttg cat tga tccaatatgt cattgcaaga aatatgaatc	578
Thr Asn Met Leu His *	
180	

tcacaatctt taacctatat atataagggtt tagattaaaa aaaaaaaaaa aaaaa	633
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<210> 11
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<400> 11	
Met Lys His Ser Leu Val Leu Ile Tyr Ala Cys Ile Ser Leu Leu Leu	
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Leu Phe His Ser Ser Leu Ser Cys Gln Leu Ile His Gln Thr Cys Lys	
20	30
Arg Ile Ala Asp Asn Asp Pro Asn Val Ser Tyr Asn Leu Cys Val Met	
35	45
Ser Leu Glu Ser Asn Pro Met Ser Ala Asn Ala Ser Leu Glu Glu Leu	
50	60
Gly Val Ile Ala Val Glu Leu Ala Leu Ser Asn Ala Thr Tyr Ile Asn	
65	80
Trp Tyr Ile Ser Asn Lys Leu Leu Gln Glu Lys Gly Phe Asp Pro Phe	
85	95
Ala Glu Ala Cys Leu Lys Asp Cys His Glu Leu Tyr Ser Asp Ala Ile	
100	110
Pro Glu Leu Lys Asp Val Leu Asp Asp Phe Lys Asp Lys Asp Tyr Tyr	
115	125
Lys Ala Asn Ile Glu Leu Ser Ala Ala Met Glu Ala Ser Ala Thr Cys	
130	140
Glu Asp Gly Tyr Lys Glu Arg Lys Gly Glu Val Ser Pro Leu Ala Lys	
145	160
Glu Asp Asn Asn Phe Phe Gln Leu Cys Ala Ile Ala Leu Ala Phe Thr	
165	175
Asn Met Leu His	
180	

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 <212> DNA
 <213> Vitis l

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gtgagctaca atttatgcgt catgagcctt gaatcaaate ccatgagtgc aaatgcgagc	180
cttgaagaac ttggagtcac cgcagtcgag ctgaccttgt ctaatgcgac atacatcaat	240

tggtacatta gcaataagct tttgcaggag aaagggtttg atccatttgc cgaggcttgc	300
ctaaaagatt gtcatgaact ttactccgac gccatccctg agttaaaga tgtgctcgat	360
gattttaagg acaaagacta ctacaaggct aatatagagt tgagcgcagc catggaggcg	420
tcggctactt gtgaagatgg ttacaaggaa aggaaagggtg aagtgtctcc cttggcaaaa	480
gaggacaaca acttctttca attgtgtgca attgctcttg ctttcactaa tatgttgc	540
tga	543

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tcccctgtct gttcaaaaac ttgggcacaa tacctctc atg ggt ttt gct ggt ttg	116
Met Gly Phe Ala Gly Leu	
1 5	

ttg ttc ctc ttt ctt ctc atg tgc ctc ctt cag tta ttt cat ccc cag	164
Leu Phe Leu Phe Leu Leu Met Ser Leu Leu Gln Leu Phe His Pro Gln	
10 15 20	

ctt gtt ctt gtg agc ggt gac tat gat ttg atc cag aaa act tgt aga	212
Leu Val Leu Val Ser Gly Asp Tyr Asp Leu Ile Gln Lys Thr Cys Arg	
25 30 35	

agc acc aaa tac tac gac ctt tgc atc tca tcc ctc aaa tct gat ccc	260
Ser Thr Lys Tyr Tyr Asp Leu Cys Ile Ser Ser Leu Lys Ser Asp Pro	
40 45 50	

aac agc ccc aat gcc gac acc aag gga ttg gcg atg att atg gtt gga	308
Asn Ser Pro Asn Ala Asp Thr Lys Gly Leu Ala Met Ile Met Val Gly	
55 60 65 70	

att gga gag gct aat gcc act gcc att tcc tct tac ttg tcc tcc caa	356
Ile Gly Glu Ala Asn Ala Thr Ala Ile Ser Ser Tyr Leu Ser Ser Gln	
75 80 85	

ttg gtc ggc tct gct aat gat tca tca atg aag aag atc ctt aag gaa	404
Leu Val Gly Ser Ala Asn Asp Ser Ser Met Lys Lys Ile Leu Lys Glu	
90 95 100	

tgc gtc aac agg tac aac tat tct agc gat gcg ctc caa gct tgc ctc	452
Cys Val Asn Arg Tyr Asn Tyr Ser Ser Asp Ala Leu Gln Ala Ser Leu	
105 110 115	

caa gct ttg acc atg gag gct tat gac tat gct tac gtg cat gtt ata	500
Gln Ala Leu Thr Met Glu Ala Tyr Asp Tyr Ala Tyr Val His Val Ile	
120 125 130	

gca gcc gca gat tat ccc aat gcc tgc cgc aat tct ttt aaa agg tgc 548
 Ala Ala Ala Asp Tyr Pro Asn Ala Cys Arg Asn Ser Phe Lys Arg Cys
 135 140 145 150

cca aga ttg cct tat cca ccg gaa ctc ggg cta aga gaa gat gtt ttg 596
 Pro Arg Leu Pro Tyr Pro Pro Glu Leu Gly Leu Arg Glu Asp Val Leu
 155 160 165

aag cat ctg tgt gat gtg gtc ttg gga att att gat ctt ctt gat tgg 644
 Lys His Leu Cys Asp Val Val Leu Gly Ile Ile Asp Leu Leu Asp Trp
 170 175 180

taa tgggtctcccc tttgcttcat tcttgggtgtt taatcaacat attgcagact 697
 *

tccaaaaata ttcgttgtgt ttctttgatc tttgtacaat gacttccacc ttgtctttga 757
 agccaaaccg tgctttgtaa ctgtagcgtt tgataagctt aaagcttata taactttatt 817
 tgtctgcaaa aaaaaaaaaa aaaaaaa 844

<210> 14
 <211> 182
 <212> PRT
 <213> Vitis L

<400> 14
 Met Gly Phe Ala Gly Leu Leu Phe Leu Phe Leu Leu Met Ser Leu Leu
 1 5 10 15
 Gln Leu Phe His Pro Gln Leu Val Leu Val Ser Gly Asp Tyr Asp Leu
 20 25 30
 Ile Gln Lys Thr Cys Arg Ser Thr Lys Tyr Tyr Asp Leu Cys Ile Ser
 35 40 45
 Ser Leu Lys Ser Asp Pro Asn Ser Pro Asn Ala Asp Thr Lys Gly Leu
 50 55 60
 Ala Met Ile Met Val Gly Ile Gly Glu Ala Asn Ala Thr Ala Ile Ser
 65 70 75 80
 Ser Tyr Leu Ser Ser Gln Leu Val Gly Ser Ala Asn Asp Ser Ser Met
 85 90 95
 Lys Lys Ile Leu Lys Glu Cys Val Asn Arg Tyr Asn Tyr Ser Ser Asp
 100 105 110
 Ala Leu Gln Ala Ser Leu Gln Ala Leu Thr Met Glu Ala Tyr Asp Tyr
 115 120 125
 Ala Tyr Val His Val Ile Ala Ala Ala Asp Tyr Pro Asn Ala Cys Arg
 130 135 140
 Asn Ser Phe Lys Arg Cys Pro Arg Leu Pro Tyr Pro Pro Glu Leu Gly
 145 150 155 160
 Leu Arg Glu Asp Val Leu Lys His Leu Cys Asp Val Val Leu Gly Ile
 165 170 175
 Ile Asp Leu Leu Asp Trp
 180

<210> 15

<211> 549
 <212> DNA
 <213> Vitis l

<400> 15
 atgggttttg ctgggtttgtt gttcctcttt cttctcatgt cgctccttca gttatttcat 60
 cccagcttg ttcttgtgag cgggtgactat gatttgatcc agaaaacttg tagaagcacc 120
 aaatactacg acctttgcat ctcatccctc aaatctgac ccaacagccc caatgccgac 180
 accaagggat tggcgatgat tatgggttga attggagagg ctaatgccac tgccatttcc 240
 tcttacttgt cctcccaatt ggtcggctct gctaagtatt catcaatgaa gaagatcctt 300
 aaggaatgag tcaacaggta caactattct agcgatgcgc tccaagcttc gctccaagct 360
 ttgacctagg aggcttatga ctatgcttac gtgcatgtta tagcagccgc agattatccc 420
 aatgcctgcc gcaattcttt taaaagggtgc ccaagattgc cttatccacc ggaactcggg 480
 ctaagagaag atgttttgaa gcatctgtgt gatgtggtct tggaattat tgatcttctt 540
 gattggtaa 549

<210> 16
 <211> 775
 <212> DNA
 <213> Vitis l

<220>
 <221> CDS
 <222> (121) ... (669)

<400> 16
 ctcatactta tagtcttaca caacatctat ctatataaag tatgtccctc tcttgatcag 60
 aaaaccaaag aagacaaaaa ggaaacagaa aaatttaagc cttgaaagtt ggaaagagcg 120
 atg agg ctt tcc tcc agt ttc ttt ctc ctc acc ctc gta ttc tta ttc 168
 Met Arg Leu Ser Ser Phe Phe Leu Leu Thr Leu Val Phe Leu Phe
 1 5 10 15

ttc atc ttt ccc gca gca acc agt tgt tgc acc aag ctc ata gat gag 216
 Phe Ile Phe Pro Ala Ala Thr Ser Cys Cys Thr Lys Leu Ile Asp Glu
 20 25 30

acc tgc aag aac tct tca cac aat gac agt aac ttc agt tac agg ttc 264
 Thr Cys Lys Asn Ser Ser His Asn Asp Ser Asn Phe Ser Tyr Arg Phe
 35 40 45

tgc aag act tcc ctc cag gca gct ccg gcc agc cgc tgc gcc agt ctc 312
 Cys Lys Thr Ser Leu Gln Ala Ala Pro Ala Ser Arg Cys Ala Ser Leu
 50 55 60

cgg gga ctg ggg ttg atc gcc atc aga tta ttc cgg gat aac gcc acc 360
 Arg Gly Leu Gly Leu Ile Ala Ile Arg Leu Phe Arg Asp Asn Ala Thr
 65 70 75 80

gac acc aga tgt ttc atc aga gaa ctg ctc gga aag aag ggg ttg gac 408
 Asp Thr Arg Cys Phe Ile Arg Glu Leu Leu Gly Lys Lys Gly Leu Asp
 85 90 95

aca tct gtg aag atg cgt ttg gaa gat tgt ttg gac atg tat tgc gat 456

Thr	Ser	Val	Lys	Met	Arg	Leu	Glu	Asp	Cys	Leu	Asp	Met	Tyr	Ser	Asp		
			100					105					110				
gga	gtc	gaa	tcc	cta	aca	cag	gcc	att	aaa	ggg	tac	agg	gct	ggg	gag		504
Gly	Val	Glu	Ser	Leu	Thr	Gln	Ala	Ile	Lys	Gly	Tyr	Arg	Ala	Gly	Glu		
			115				120					125					
tat	ttc	gat	gct	aat	gtc	caa	ggt	tcg	ggg	gct	atg	act	tat	gct	agt		552
Tyr	Phe	Asp	Ala	Asn	Val	Gln	Val	Ser	Gly	Ala	Met	Thr	Tyr	Ala	Ser		
			130				135				140						
act	tgt	gaa	gat	ggg	ttc	cag	gag	aag	gaa	ggg	ttg	ggt	tcg	ccg	ttg		600
Thr	Cys	Glu	Asp	Gly	Phe	Gln	Glu	Lys	Glu	Gly	Leu	Val	Ser	Pro	Leu		
						150				155					160		
acg	aag	caa	aac	gac	gat	gct	ttt	cag	ttg	ggg	gcg	ctc	tct	ctt	tcg		648
Thr	Lys	Gln	Asn	Asp	Asp	Ala	Phe	Gln	Leu	Gly	Ala	Leu	Ser	Leu	Ser		
				165				170					175				
att	atg	aat	aag	cag	aag	tga	ttcatggctg	gctgattggc	tggttttgg								699
Ile	Met	Asn	Lys	Gln	Lys	*											
				180													
ttttttta	aat	tctgagg	caa	tgcttctctt	tttctaa	ata	attaatattt	actttcacaa									759
aaaaaaaa	aaaaaa																775

<210> 17
 <211> 182
 <212> PRT
 <213> Vitis 1

<400> 17

Met	Arg	Leu	Ser	Ser	Ser	Phe	Phe	Leu	Leu	Thr	Leu	Val	Phe	Leu	Phe		
1				5					10					15			
Phe	Ile	Phe	Pro	Ala	Ala	Thr	Ser	Cys	Cys	Thr	Lys	Leu	Ile	Asp	Glu		
			20					25					30				
Thr	Cys	Lys	Asn	Ser	Ser	His	Asn	Asp	Ser	Asn	Phe	Ser	Tyr	Arg	Phe		
		35				40					45						
Cys	Lys	Thr	Ser	Leu	Gln	Ala	Ala	Pro	Ala	Ser	Arg	Cys	Ala	Ser	Leu		
	50				55					60							
Arg	Gly	Leu	Gly	Leu	Ile	Ala	Ile	Arg	Leu	Phe	Arg	Asp	Asn	Ala	Thr		
65				70					75					80			
Asp	Thr	Arg	Cys	Phe	Ile	Arg	Glu	Leu	Leu	Gly	Lys	Lys	Gly	Leu	Asp		
			85					90					95				
Thr	Ser	Val	Lys	Met	Arg	Leu	Glu	Asp	Cys	Leu	Asp	Met	Tyr	Ser	Asp		
			100					105					110				
Gly	Val	Glu	Ser	Leu	Thr	Gln	Ala	Ile	Lys	Gly	Tyr	Arg	Ala	Gly	Glu		
		115				120						125					
Tyr	Phe	Asp	Ala	Asn	Val	Gln	Val	Ser	Gly	Ala	Met	Thr	Tyr	Ala	Ser		
	130				135					140							
Thr	Cys	Glu	Asp	Gly	Phe	Gln	Glu	Lys	Glu	Gly	Leu	Val	Ser	Pro	Leu		
145				150						155					160		
Thr	Lys	Gln	Asn	Asp	Asp	Ala	Phe	Gln	Leu	Gly	Ala	Leu	Ser	Leu	Ser		

Ile Met Asn Lys Lys Gln Lys
180

165

170

175

<210> 18
<211> 549
<212> DNA
<213> Vitis l

<400> 18
atgaggcttt cctccagttt ctttctcttc accctcgtat tcttattctt catctttccc 60
gcagcaacca gttgttgac caagctcata gatgagacct gcaagaactc ttcacacaat 120
gacagtaact tcagttacag gttctgcaag acttccctcc aggcagctcc ggccagccgc 180
tgccgagctc tccggggact ggggttgatc gccatcagat tattccggga taacgccacc 240
gacaccagat gtttcatcag agaactgctc ggaaagaagg ggttggacac atctgtgaag 300
atgcgtttgg aagattgttt ggacatgtat tcggatggag tcgaatccct aacacaggcc 360
attaaagggt acagggctgg ggagtatttc gatgctaattg tccaagtctc ggggtgctatg 420
acttatgcta gtacttgta agatggtttc caggagaagg aagggttggt ttcgccgttg 480
acgaagcaaa acgacgatgc ttttcagttg ggtgcgctct ctctttcgat tatgaataag 540
cagaagtga 549

<210> 19
<211> 686
<212> DNA
<213> Vitis L

<220>
<221> CDS
<222> (11) ... (547)

<400> 19
gctatcatcc atg gct tct gta att ctt ctt ttt ctt ctc act ctt tca 49
Met Ala Ser Val Ile Leu Leu Phe Leu Leu Thr Leu Ser
1 5 10
tcc cct ctc ttc ttt ggc caa aca ctc aac ccc gta gag gca gga gac 97
Ser Pro Leu Phe Phe Gly Gln Thr Leu Asn Pro Val Glu Ala Gly Asp
15 20 25
aaa cta att gaa agt gca tgc cac act gct gag gta cca gta gta tgc 145
Lys Leu Ile Glu Ser Ala Cys His Thr Ala Glu Val Pro Val Val Cys
30 35 40 45
atg cag tgt gta aaa tct gac gag cgt tcg ggg aaa gcc gat gcg gta 193
Met Gln Cys Val Lys Ser Asp Glu Arg Ser Gly Lys Ala Asp Ala Val
50 55 60
ggg att gcc aac atc atc gtc gac tgt ttg atg agc cac tct agc tac 241
Gly Ile Ala Asn Ile Ile Val Asp Cys Leu Met Ser His Ser Ser Tyr
65 70 75
ttg gca agc aac atg tcg aat tta ggt tct aat cct gaa cac aat gcc 289
Leu Ala Ser Asn Met Ser Asn Leu Gly Ser Asn Pro Glu His Asn Ala

80	85	90	
aca aaa tca gcc tat gaa cat tgc ttc ctg cac tgt tct gat gca aag			337
Thr Lys Ser Ala Tyr Glu His Cys Phe Leu His Cys Ser Asp Ala Lys			
95	100	105	
aag gcg cta aat tca gca gct ttg gag cta aag aat ggc agc tat gat			385
Lys Ala Leu Asn Ser Ala Ala Leu Glu Leu Lys Asn Gly Ser Tyr Asp			
110	115	120	125
agc gct gaa ctg tcc ttg cgc gaa gca gcg cta tat caa ggc aca tgc			433
Ser Ala Glu Leu Ser Leu Arg Glu Ala Ala Leu Tyr Gln Gly Thr Cys			
130	135	140	
cga tac gag ttt gtg agt tca aat gag act tat gtg cca cct aat gtt			481
Arg Tyr Glu Phe Val Ser Ser Asn Glu Thr Tyr Val Pro Pro Asn Val			
145	150	155	
tac tat gat ctg aag gtc ttt gat ata ctt act gtg gct gcc ttt aga			529
Tyr Tyr Asp Leu Lys Val Phe Asp Ile Leu Thr Val Ala Ala Phe Arg			
160	165	170	
att ata gag aag ctt tga ttaagagttt tggagggttt tcacctaatt			577
Ile Ile Glu Lys Leu *			
175			
gctcatcatc catgaaaaat aaagtttcat gttgactagt agacatgtaa catgaaatat			637
tgagacataa catacacctc cttatcatct aaaaaaaaaa aaaaaaaaaa			686

<210> 20
 <211> 178
 <212> PRT
 <213> Vitis L

<400> 20

Met Ala Ser Val	Ile Leu Leu Phe Leu Leu Thr Leu Ser Ser Pro Leu
1	5 10 15
Phe Phe Gly Gln Thr Leu Asn Pro Val Glu Ala Gly Asp Lys Leu Ile	
20	25 30
Glu Ser Ala Cys His Thr Ala Glu Val Pro Val Val Cys Met Gln Cys	
35	40 45
Val Lys Ser Asp Glu Arg Ser Gly Lys Ala Asp Ala Val Gly Ile Ala	
50	55 60
Asn Ile Ile Val Asp Cys Leu Met Ser His Ser Ser Tyr Leu Ala Ser	
65	70 75 80
Asn Met Ser Asn Leu Gly Ser Asn Pro Glu His Asn Ala Thr Lys Ser	
85	90 95
Ala Tyr Glu His Cys Phe Leu His Cys Ser Asp Ala Lys Lys Ala Leu	
100	105 110
Asn Ser Ala Ala Leu Glu Leu Lys Asn Gly Ser Tyr Asp Ser Ala Glu	
115	120 125
Leu Ser Leu Arg Glu Ala Ala Leu Tyr Gln Gly Thr Cys Arg Tyr Glu	
130	135 140

Phe Val Ser Ser Asn Glu Thr Tyr Val Pro Pro Asn Val Tyr Tyr Asp
 145 150 155 160
 Leu Lys Val Phe Asp Ile Leu Thr Val Ala Ala Phe Arg Ile Ile Glu
 165 170 175
 Lys Leu

<210> 21
 <211> 537
 <212> DNA
 <213> Vitis 1

<400> 21
 atggcttctg taattcttct ttttcttctc actctttcat cccctctctt ctttggccaa 60
 aactcaacc ccgtagaggc aggagacaaa ctaattgaaa gtgcatgcc cactgctgag 120
 gtaccagtag tatgcatgca gtgtgtaaaa tctgacgagc gttcggggaa agccgatgcg 180
 gtagggattg ccaacatcat cgtcgactgt ttgatgagcc actctagcta cttggcaagc 240
 aacatgtcga atttagggtc taatcctgaa cacaatgcc caaaatcagc ctatgaacat 300
 tgcttcctgc actgttctga tgcaaagaag gcgctaaatt cagcagcttt ggagctaaag 360
 aatggcagct atgatagcgc tgaactgtcc ttgcgcgaag cagcgctata tcaaggcaca 420
 tgccgatacg agtttgtgag ttcaaagtag acttatgtgc cacctaagtg ttactatgat 480
 ctgaagggtc ttgatatact tactgtggct gccttttagaa ttatagagaa gctttga 537

<210> 22
 <211> 709
 <212> DNA
 <213> Vitis 1

<220>
 <221> CDS
 <222> (13)...(558)

<400> 22
 gaaattaagg aa atg gct tcc ttg agt ggg gta ctg tta ctt gtt cat atc 51
 Met Ala Ser Leu Ser Gly Val Leu Leu Val His Ile
 1 5 10
 tcc ctc atg gcc acc act ctc ttc tac tat cct tca cat gcg atc gga 99
 Ser Leu Met Ala Thr Thr Leu Phe Tyr Tyr Pro Ser His Ala Ile Gly
 15 20 25
 caa gac gtc gtc gag cag gta tgc cag caa acg gag gac tat caa ttc 147
 Gln Asp Val Val Glu Gln Val Cys Gln Gln Thr Glu Asp Tyr Gln Phe
 30 35 40 45
 tgt ttc aat acc atc ctc aga gat cct cgg act ccg gca gtt aac atg 195
 Cys Phe Asn Thr Ile Leu Arg Asp Pro Arg Thr Pro Ala Val Asn Met
 50 55 60
 gag ggg ctg tgc ctc ctc agt gtg gca ata acc ata gac cac gtt agg 243
 Glu Gly Leu Cys Leu Leu Ser Val Ala Ile Thr Ile Asp His Val Arg
 65 70 75

gaa gcg gtg gat aaa ata ccg ggg ctg ctg gag aaa gct act gat cca	291
Glu Ala Val Asp Lys Ile Pro Gly Leu Leu Glu Lys Ala Thr Asp Pro	
80 85 90	
gtg gac aag caa aga atg acg act tgc caa tcc aac tat gga gca gcg	339
Val Asp Lys Gln Arg Met Thr Thr Cys Gln Ser Asn Tyr Gly Ala Ala	
95 100 105	
gcg ggg gac ttc cag agg gcg tgg ggc tgc gct tct tca aag gct ttc	387
Ala Gly Asp Phe Gln Arg Ala Trp Gly Ser Ala Ser Ser Lys Ala Phe	
110 115 120 125	
cat gat gtg ctg ggc tgg gtt cag aag gga agt ggt cag gtt ata aac	435
His Asp Val Leu Gly Trp Val Gln Lys Gly Ser Gly Gln Val Ile Asn	
130 135 140	
tgt gaa aat ata tac cgg caa agt ccg ccg atc cgt gaa tct ccc ctc	483
Cys Glu Asn Ile Tyr Arg Gln Ser Pro Pro Ile Arg Glu Ser Pro Leu	
145 150 155	
aca gtt gac aac cac aac gtg att aaa tta gca gga att act ttg gtt	531
Thr Val Asp Asn His Asn Val Ile Lys Leu Ala Gly Ile Thr Leu Val	
160 165 170	
gtt ctt ggt atg ctt ggt gtt cgt tga agatggtgtg tcttccttga	578
Val Leu Gly Met Leu Gly Val Arg *	
175 180	
ggtaaagctc acgttcttgg aattaacgta caataaatgt ggaatgcaat actggttggt	638
gggtcaataaaa aactgatgtg aatttactac tcaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	698
aaaaaaaaaaaa a	709

<210> 23
 <211> 181
 <212> PRT
 <213> Vitis 1

<400> 23

Met Ala Ser Leu Ser Gly Val Leu Leu Leu Val His Ile Ser Leu Met	
1 5 10 15	
Ala Thr Thr Leu Phe Tyr Tyr Pro Ser His Ala Ile Gly Gln Asp Val	
20 25 30	
Val Glu Gln Val Cys Gln Gln Thr Glu Asp Tyr Gln Phe Cys Phe Asn	
35 40 45	
Thr Ile Leu Arg Asp Pro Arg Thr Pro Ala Val Asn Met Glu Gly Leu	
50 55 60	
Cys Leu Leu Ser Val Ala Ile Thr Ile Asp His Val Arg Glu Ala Val	
65 70 75 80	
Asp Lys Ile Pro Gly Leu Leu Glu Lys Ala Thr Asp Pro Val Asp Lys	
85 90 95	
Gln Arg Met Thr Cys Gln Ser Asn Tyr Gly Ala Ala Ala Gly Asp	
100 105 110	
Phe Gln Arg Ala Trp Gly Ser Ala Ser Ser Lys Ala Phe His Asp Val	

115	120	125
Leu Gly Trp Val Gln Lys Gly Ser Gly Gln Val Ile Asn Cys Glu Asn		
130	135	140
Ile Tyr Arg Gln Ser Pro Ile Arg Glu Ser Pro Leu Thr Val Asp		
145	150	155
Asn His Asn Val Ile Lys Leu Ala Gly Ile Thr Leu Val Val Leu Gly		160
	165	170
Met Leu Gly Val Arg		175
	180	

<210> 24
 <211> 546
 <212> DNA
 <213> Vitis l

<400> 24

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ttctactatc	cttcacatgc	gatcggacaa	gacgtcgtcg	agcaggtatg	ccagcaaacg	120
gaggactatc	aattctgttt	caataccatc	ctcagagatc	ctcggactcc	ggcagttaac	180
atggaggggc	tgtgcctcct	cagtgtggca	ataaccatag	accacgttag	ggaagcgggtg	240
gataaaatac	cggggctgct	ggagaaaagt	actgatccag	tggacaagca	aagaatgacg	300
acttgccaat	ccaactatgg	agcagcggcg	ggggacttcc	agagggcgtg	gggctcggct	360
tcttcaaagg	ctttccatga	tgtgctgggc	tgggttcaga	aggggaagtgg	tcaggttata	420
aactgtgaaa	atatataccg	gcaaagtccg	ccgatccgtg	aatctcccct	cacagttgac	480
aaccacaacg	tgattaaatt	agcaggaatt	actttgggtg	ttcttggtat	gcttggtggt	540
cgttga						546

<210> 25
 <211> 1067
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (68) ... (691)

<400> 25

tagacatata	ccaacggtaa	cgtgttgcat	cccattgtaa	aagccggcta	tcactttcag	60
ggacaaa	atg ccc aca tta att att ata aaa ggc cgg cca aat atg gct					109
	Met Pro Thr Leu Ile Ile Ile Lys Gly Arg Pro Asn Met Ala					
	1	5	10			
tcc gga acg ccc tac act gcc gtc ggc gtc atc ttc ctc tcc gtc ttc						157
Ser Gly Thr Pro Tyr Thr Ala Val Gly Val Ile Phe Leu Ser Val Phe						
15	20	25	30			
ctc gtc gcc gcg gca tcc gca ggc cgc acc gcg gca cct gcg gcc gcg						205
Leu Val Ala Ala Ala Ser Ala Gly Arg Thr Ala Ala Pro Ala Ala Ala						
	35	40	45			
ccg tcg agc aag tac tcg ctc gag gaa gcg tgc gag cag acc gcg ggg						253
Pro Ser Ser Lys Tyr Ser Leu Glu Glu Ala Cys Glu Gln Thr Ala Gly						
	50	55	60			

cac gag gac ctg tgc gtg gag acg ctg tcc gcg gac ccg tcg tcc aag	301
His Glu Asp Leu Cys Val Glu Thr Leu Ser Ala Asp Pro Ser Ser Lys	
65 70 75	
act gcc gac act acg ggg ctc gca cgg ttg gcc atc cag gcg gca cag	349
Thr Ala Asp Thr Thr Gly Leu Ala Arg Leu Ala Ile Gln Ala Ala Gln	
80 85 90	
cgg aac gcg tcg gag acg gcg acc tac ctc tcc agc atc tac gac gac	397
Arg Asn Ala Ser Glu Thr Ala Thr Tyr Leu Ser Ser Ile Tyr Asp Asp	
95 100 105 110	
gac agc ctt gag aac aag acg gcg cag ctg cag cag tgc ctt gaa aac	445
Asp Ser Leu Glu Asn Lys Thr Ala Gln Leu Gln Gln Cys Leu Glu Asn	
115 120 125	
tgc ggc gag agg tac gag tcg gcg gtg gag cag ctg tcg gac gcg acg	493
Cys Gly Glu Arg Tyr Glu Ser Ala Val Glu Gln Leu Ser Asp Ala Thr	
130 135 140	
tcg gcg ctg gac acg ggc gcg tac agc gag tcg gag gag ctg gtg gtg	541
Ser Ala Leu Asp Thr Gly Ala Tyr Ser Glu Ser Glu Glu Leu Val Val	
145 150 155	
gcg agc cag gct gag gtg agg ctg tgt cag cgt ggc tgc caa gcc gtg	589
Ala Ser Gln Ala Glu Val Arg Leu Cys Gln Arg Gly Cys Gln Ala Val	
160 165 170	
ccg aac cac cgc aac atc ctc tcg gcg cgc aac cgc aac gtc gac cag	637
Pro Asn His Arg Asn Ile Leu Ser Ala Arg Asn Arg Asn Val Asp Gln	
175 180 185 190	
ctc tgc agc atc gcg ctc gcc atc acc aag ctc atc cac gga ccg cca	685
Leu Cys Ser Ile Ala Leu Ala Ile Thr Lys Leu Ile His Gly Pro Pro	
195 200 205	
tct tga tacacaggac gtagtaaaca tttagggtt gttcatttcg ccgttaatcc	741
Ser *	

atgtggattg ggtggtattg agtcggttta attccatagc aagtcaaaat acatcccaat	801
ccatcccaat acacaccaat acacatggaa ttgaagggtg ttccatactt gtaacgtaat	861
tggttaactaa tgatgacgtt aaatcatatt tgtttaagtt taattataat cagataccac	921
ataaaaaaatt aatatcagac tatttaaatt tattaccgct ggtattcaag tgtgaatcat	981
gtggctatat caacttctat tgtaagcaga ttgagagtag tcggtgggta accatattaa	1041
attaaaaaaaa aaaaaaaaaa aaaaaa	1067

<210> 26
 <211> 207
 <212> PRT
 <213> Zea mays

<400> 26

Met	Pro	Thr	Leu	Ile	Ile	Ile	Lys	Gly	Arg	Pro	Asn	Met	Ala	Ser	Gly
1				5					10					15	
Thr	Pro	Tyr	Thr	Ala	Val	Gly	Val	Ile	Phe	Leu	Ser	Val	Phe	Leu	Val
			20					25					30		
Ala	Ala	Ala	Ser	Ala	Gly	Arg	Thr	Ala	Ala	Pro	Ala	Ala	Ala	Pro	Ser
		35					40					45			
Ser	Lys	Tyr	Ser	Leu	Glu	Glu	Ala	Cys	Glu	Gln	Thr	Ala	Gly	His	Glu
	50				55						60				
Asp	Leu	Cys	Val	Glu	Thr	Leu	Ser	Ala	Asp	Pro	Ser	Ser	Lys	Thr	Ala
65				70						75					80
Asp	Thr	Thr	Gly	Leu	Ala	Arg	Leu	Ala	Ile	Gln	Ala	Ala	Gln	Arg	Asn
			85					90						95	
Ala	Ser	Glu	Thr	Ala	Thr	Tyr	Leu	Ser	Ser	Ile	Tyr	Asp	Asp	Asp	Ser
			100					105					110		
Leu	Glu	Asn	Lys	Thr	Ala	Gln	Leu	Gln	Gln	Cys	Leu	Glu	Asn	Cys	Gly
		115					120					125			
Glu	Arg	Tyr	Glu	Ser	Ala	Val	Glu	Gln	Leu	Ser	Asp	Ala	Thr	Ser	Ala
	130					135					140				
Leu	Asp	Thr	Gly	Ala	Tyr	Ser	Glu	Ser	Glu	Glu	Leu	Val	Val	Ala	Ser
145					150					155					160
Gln	Ala	Glu	Val	Arg	Leu	Cys	Gln	Arg	Gly	Cys	Gln	Ala	Val	Pro	Asn
			165					170						175	
His	Arg	Asn	Ile	Leu	Ser	Ala	Arg	Asn	Arg	Asn	Val	Asp	Gln	Leu	Cys
		180						185					190		
Ser	Ile	Ala	Leu	Ala	Ile	Thr	Lys	Leu	Ile	His	Gly	Pro	Pro	Ser	
		195					200					205			

<210> 27

<211> 624

<212> DNA

<213> Zea mays

<400> 27

atgccacat	taattattat	aaaaggccgg	ccaaatatgg	cttcggaac	gccctacact	60
gccgtggcg	tcattcttct	ctcgtcttct	ctcgtcgccg	cgcatccgc	aggccgcacc	120
gcgccacctg	cgccgcgcgc	gtcgagcaag	tactcgctcg	aggaagcgtg	cgagcagacc	180
gcggggcacg	aggacctgtg	cgtggagacg	ctgtccgcgg	accgctcgtc	caagactgcc	240
gacactacgg	ggctcgacacg	gttgcccatc	caggcggcac	agcggaacgc	gtcggagacg	300
gcgacctacc	tctccagcat	ctacgacgac	gacagccttg	agaacaagac	ggcgagctg	360
cagcagtgcc	ttgaaaactg	cggcgagagg	tacgagtcgg	cggaggagca	gctgtcggac	420
gcgacgtcgg	cgctggacac	gggcgcgtac	agcgagtcgg	aggagctggt	ggtggcgagc	480
caggctgagg	tgaggctgtg	tcagcgtggc	tgccaagccg	tgccgaacca	ccgcaacatc	540
ctctcggcgc	gcaaccgcaa	cgtcgaccag	ctctgcagca	tcgcgctcgc	catcaccaag	600
ctcatccacg	gaccgccatc	ttga				624

<210> 28

<211> 1214

<212> DNA

<213> Oryza sativa

<220>

<221> CDS

<222> (124) ... (810)

<400> 28

aactagctat ctagcttagc ctcgctaaac caacaccatc gtaaaaaatct ctttgatagt	60
tgacatcgag gcagtgatta attaagtagc tagctagtta caggcacaag gagagaaaca	120
cca atg gca tca atg gcg cca tcg gca atg gtg ctc atc gtc ctc ctc	168
Met Ala Ser Met Ala Pro Ser Ala Met Val Leu Ile Val Leu Leu	
1 5 10 15	
gtc ctg gtg gtt ctc ccg tcg agc act ctg tgc tca cgg gcg ggg cct	216
Val Leu Val Val Leu Pro Ser Ser Thr Leu Cys Ser Arg Ala Gly Pro	
20 25 30	
tct tcc aag cac ggc cat ggc ggt ggc cac gcc aag cgc gtg ccg cca	264
Ser Ser Lys His Gly His Gly Gly Gly His Ala Lys Arg Val Pro Pro	
35 40 45	
ccg gcg tcg gta ccg ccg ccg ccg ccg ccg cca cca gcg ccg gcg gcg	312
Pro Ala Ser Val Pro Pro Pro Pro Pro Pro Pro Ala Pro Ala Ala	
50 55 60	
ctg gtg cgt gcc acc tgc aac tcc acc tcc tac tac gac ctc tgc gtc	360
Leu Val Arg Ala Thr Cys Asn Ser Thr Ser Tyr Tyr Asp Leu Cys Val	
65 70 75	
gcc gag ctg tcc gcc gac ccg tcg agc gcc acg gcc gac gtg cgc gga	408
Ala Glu Leu Ser Ala Asp Pro Ser Ser Ala Thr Ala Asp Val Arg Gly	
80 85 90 95	
ctg tcg tcc atc gcc gtc tcc gcc gcc gcc gcc aac gca tcc ggg gcg	456
Leu Ser Ser Ile Ala Val Ser Ala Ala Ala Ala Asn Ala Ser Gly Ala	
100 105 110	
gcg cag gcg gcc tcg gcg ctg gcg aac gcg acc gac gcg ggg acg acg	504
Ala Gln Ala Ala Ser Ala Leu Ala Asn Ala Thr Asp Ala Gly Thr Thr	
115 120 125	
gcg ggc gtc gcc ggc gac ggc ggc ggc gca gtc gta cag agg ctg ctc	552
Ala Gly Val Ala Gly Asp Gly Gly Gly Ala Val Val Gln Arg Leu Leu	
130 135 140	
gcc acc tgc gcg gcc aag tac ggc gac gcc cgc gac gcg ctc gcc gcg	600
Ala Thr Cys Ala Ala Lys Tyr Gly Asp Ala Arg Asp Ala Leu Ala Ala	
145 150 155	
gcc aag ggc tcg atc gcg cag cag gac tac gac atg gcg tcc gtg cac	648
Ala Lys Gly Ser Ile Ala Gln Gln Asp Tyr Asp Met Ala Ser Val His	
160 165 170 175	
gtc agc gcc gcc gcg gag tac ccg cag gtg tgc agg acg ctg ttc ggg	696
Val Ser Ala Ala Ala Glu Tyr Pro Gln Val Cys Arg Thr Leu Phe Gly	
180 185 190	

cgg cag agc ccc gga gac tac ccg ccg gag ctc gcc gcg aca gag gtg	744
Arg Gln Ser Pro Gly Asp Tyr Pro Pro Glu Leu Ala Ala Thr Glu Val	
195 200 205	

gcg ctc agg cag ctc tgc tcc gtc gcg ctc gac atc atc gcg ctc ctc	792
Ala Leu Arg Gln Leu Cys Ser Val Ala Leu Asp Ile Ile Ala Leu Leu	
210 215 220	

agc tca tcc agc aac tag cagctctgct tgttaccgag ctcaagttca	840
Ser Ser Ser Ser Asn *	
225	

cccaaccagc taactactcg caattcgtat aggtacaaat ggtgcaaata tagtactgta	900
taatactact gcatagaata catatacgtg taatgacacg tatttatctt ttttttttgc	960
aaggggacag tatatcaatt aattgtgtgt cccaattaat tagagtcgaa tccacttgat	1020
atgttctttt gtttaattgt attatcactc catagaggag ttgctgtagt agtgcaaaag	1080
gtacatgcgg ccgcccgcag tatgcatgta tttcacttct gtttcagtat aataatggct	1140
attcaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1200
aaaaaaaaaa aaaa	1214

<210> 29
 <211> 228
 <212> PRT
 <213> Oryza sativa

<400> 29	
Met Ala Ser Met Ala Pro Ser Ala Met Val Leu Ile Val Leu Leu Val	
1 5 10 15	
Leu Val Val Leu Pro Ser Ser Thr Leu Cys Ser Arg Ala Gly Pro Ser	
20 25 30	
Ser Lys His Gly His Gly Gly Gly His Ala Lys Arg Val Pro Pro Pro	
35 40 45	
Ala Ser Val Pro Pro Pro Pro Pro Pro Pro Ala Pro Ala Ala Leu	
50 55 60	
Val Arg Ala Thr Cys Asn Ser Thr Ser Tyr Tyr Asp Leu Cys Val Ala	
65 70 75 80	
Glu Leu Ser Ala Asp Pro Ser Ser Ala Thr Ala Asp Val Arg Gly Leu	
85 90 95	
Ser Ser Ile Ala Val Ser Ala Ala Ala Ala Asn Ala Ser Gly Ala Ala	
100 105 110	
Gln Ala Ala Ser Ala Leu Ala Asn Ala Thr Asp Ala Gly Thr Thr Ala	
115 120 125	
Gly Val Ala Gly Asp Gly Gly Gly Ala Val Val Gln Arg Leu Leu Ala	
130 135 140	
Thr Cys Ala Ala Lys Tyr Gly Asp Ala Arg Asp Ala Leu Ala Ala Ala	
145 150 155 160	
Lys Gly Ser Ile Ala Gln Gln Asp Tyr Asp Met Ala Ser Val His Val	
165 170 175	
Ser Ala Ala Ala Glu Tyr Pro Gln Val Cys Arg Thr Leu Phe Gly Arg	
180 185 190	
Gln Ser Pro Gly Asp Tyr Pro Pro Glu Leu Ala Ala Thr Glu Val Ala	
195 200 205	
Leu Arg Gln Leu Cys Ser Val Ala Leu Asp Ile Ile Ala Leu Leu Ser	

210
Ser Ser Ser Asn
225

215

220

<210> 30
<211> 687
<212> DNA
<213> Oryza sativa

<400> 30
atggcatcaa tggcgccatc ggcaatggtg ctcacgtgcc tcctcgctct ggtggttctc 60
ccgtcgagca ctctgtgctc acgggcgggg ccttcttcca agcacggcca tggcggtggc 120
cacgccaagc gcgtgccgcc accggcgctc gtaccgccgc cgcgcgcgcc gccaccagcg 180
ccggcgggcg tggcgcgctg cacctgcaac tccacctct actacgacct ctgcgtcgcc 240
gagctgtccg ccgaccgctc gagcgccacg gccgacgtgc gcggactgtc gtccatcgcc 300
gtctccgccg ccgcccgaac cgcacccggg gcggcgacgg cggcctcggc gctggcgaaac 360
gcgaccgacg cggggacgac ggcgggcgct gccggcgacg gcggcgggcg agtcgtacag 420
aggctgtctg ccacctgcgc ggccaagtac ggcgacgccc gcgacgcgct cgcgcgcgcc 480
aagggtcga tcgcgcagca ggactacgac atggcgctcg tgcacgtcag cgcgcgcgcg 540
gagtaccgac aggtgtgcag gacgctgttc gggcggcaga gccccggaga ctaccgcgcg 600
gagctcgccg cgacagaggt ggcgctcagg cagctctgct ccgtcgcgct cgacatcacc 660
gcgctctca gtcacatccag caactag 687

<210> 31
<211> 782
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (81)...(620)

<400> 31
attgtctct cctttttcac cctctctccc cctcaaaaaa tctcaagata ccaattagca 60
cctcctata ctaatctata atg gct tct tct aag atc atc ttc ata ttt ctc 113
Met Ala Ser Ser Lys Ile Ile Phe Ile Phe Leu
1 5 10
ctc ttt cta gca cac ctt cat caa cat aca ttt gtg aaa gga gat tcc 161
Leu Phe Leu Ala His Leu His Gln His Thr Phe Val Lys Gly Asp Ser
15 20 25
agt ttg ata aag aga act tgc aag aac acc aag tac tac aat cta tgc 209
Ser Leu Ile Lys Arg Thr Cys Lys Asn Thr Lys Tyr Tyr Asn Leu Cys
30 35 40
ttc tct tcc ctc aaa tct gat cct agc agt cca aac gca gat cct aag 257
Phe Ser Ser Leu Lys Ser Asp Pro Ser Ser Pro Asn Ala Asp Pro Lys
45 50 55
ggc cta gct gtg atc atg att ggg att gga atg acc aat gcc act tcc 305
Gly Leu Ala Val Ile Met Ile Gly Ile Gly Met Thr Asn Ala Thr Ser
60 65 70 75

act tct tcc tac ttg tct tca aag ttg ctt agc ccc tcc aac aac aca 353
 Thr Ser Ser Tyr Leu Ser Ser Lys Leu Leu Ser Pro Ser Asn Asn Thr
 80 85 90

acc ttg aaa agg gtc cta aag gag tgt gca gat aag tac tca tat gct 401
 Thr Leu Lys Arg Val Leu Lys Glu Cys Ala Asp Lys Tyr Ser Tyr Ala
 95 100 105

ggg gat gcc ctc caa gat tcg gtt cag gat ttg gct aat gag gct tat 449
 Gly Asp Ala Leu Gln Asp Ser Val Gln Asp Leu Ala Asn Glu Ala Tyr
 110 115 120

gac tat gct tac atg cac atc act gcc gcc aaa gat tac cca aat gct 497
 Asp Tyr Ala Tyr Met His Ile Thr Ala Ala Lys Asp Tyr Pro Asn Ala
 125 130 135

tgc cac aac gct ttc aaa cgg tac ccc ggt ttg gct tat cct cgt gat 545
 Cys His Asn Ala Phe Lys Arg Tyr Pro Gly Leu Ala Tyr Pro Arg Asp
 140 145 150 155

ctt gct agt aga gaa gat ggt ttg aag cat ata tgt gat gtg gca atg 593
 Leu Ala Ser Arg Glu Asp Gly Leu Lys His Ile Cys Asp Val Ala Met
 160 165 170

ggg att ata gat aat ctt gat tgg tag gtgcatgcat ttgagtatat 640
 Gly Ile Ile Asp Asn Leu Asp Trp *
 175

agcttccagt ttgttgtgca aaccatgtta tatctctggt gttatgtttg gttactatgt 700
 attgttaagt tcttggtata atatattaat gggaacaaaa ttttagtatt tgtttagaaa 760
 aaaaaaaaaa aaaaaaaaaa aa 782

<210> 32
 <211> 179
 <212> PRT
 <213> Glycine max

<400> 32
 Met Ala Ser Ser Lys Ile Ile Phe Ile Phe Leu Leu Phe Leu Ala His
 1 5 10 15
 Leu His Gln His Thr Phe Val Lys Gly Asp Ser Ser Leu Ile Lys Arg
 20 25 30
 Thr Cys Lys Asn Thr Lys Tyr Tyr Asn Leu Cys Phe Ser Ser Leu Lys
 35 40 45
 Ser Asp Pro Ser Ser Pro Asn Ala Asp Pro Lys Gly Leu Ala Val Ile
 50 55 60
 Met Ile Gly Ile Gly Met Thr Asn Ala Thr Ser Thr Ser Ser Tyr Leu
 65 70 75 80
 Ser Ser Lys Leu Leu Ser Pro Ser Asn Asn Thr Thr Leu Lys Arg Val
 85 90 95
 Leu Lys Glu Cys Ala Asp Lys Tyr Ser Tyr Ala Gly Asp Ala Leu Gln
 100 105 110

aac gca gat cct aag ggc cta gct gtg atc atg att gga ata gga atg	308
Asn Ala Asp Pro Lys Gly Leu Ala Val Ile Met Ile Gly Ile Gly Met	
55 60 65 70	
acc aat gcc act tcc aca tcc tcc tac ttg tct tca aag ttg cct acc	356
Thr Asn Ala Thr Ser Thr Ser Ser Tyr Leu Ser Ser Lys Leu Pro Thr	
75 80 85	
ccc tcc aac aac aca acc tgg aaa agg gtc ctc aag gag tgt gct gat	404
Pro Ser Asn Asn Thr Thr Trp Lys Arg Val Leu Lys Glu Cys Ala Asp	
90 95 100	
aag tac tcc tat gct ggt gat gcc ctc caa gat tgc gtg cag gat ttg	452
Lys Tyr Ser Tyr Ala Gly Asp Ala Leu Gln Asp Ser Val Gln Asp Leu	
105 110 115	
gct aat gag gct tat gac tat gct tac atg cac atc act gcc gcc aaa	500
Ala Asn Glu Ala Tyr Asp Tyr Ala Tyr Met His Ile Thr Ala Ala Lys	
120 125 130	
gat tac cca aat gct tgc cac aac gct ttc aaa cgg tac cct ggt ttg	548
Asp Tyr Pro Asn Ala Cys His Asn Ala Phe Lys Arg Tyr Pro Gly Leu	
135 140 145 150	
gtt tat cct cgt gat ctt gct cgt aga gaa gat ggt ttg aag cat ata	596
Val Tyr Pro Arg Asp Leu Ala Arg Arg Glu Asp Gly Leu Lys His Ile	
155 160 165	
tgc gat gtg gca atg ggg att ata gat aat ctt gat tgg tag	638
Cys Asp Val Ala Met Gly Ile Ile Asp Asn Leu Asp Trp *	
170 175	
gtgcatgcat ttgagtatat agcttccagt ttgttatgca aaccatgtta tatctctggt	698
gttatgtttg gctaccttgt atcttggttaa ttatgttctt ggtataatat attggacata	758
aatgttttag tctttttgaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa	814

<210> 35

<211> 179

<212> PRT

<213> Glycine max

<400> 35

Met Val Ser Ser Lys Ile Phe Phe Leu Phe Leu Leu Phe Leu Ala His	
1 5 10 15	
Leu His Gln His Ala Ser Val Glu Gly Asp Ser Ser Leu Ile Lys Arg	
20 25 30	
Thr Cys Lys Asn Thr Lys Tyr Tyr Asn Leu Cys Phe Ser Ser Leu Lys	
35 40 45	
Ser Asp Pro Ser Ser Pro Asn Ala Asp Pro Lys Gly Leu Ala Val Ile	
50 55 60	
Met Ile Gly Ile Gly Met Thr Asn Ala Thr Ser Thr Ser Ser Tyr Leu	
65 70 75 80	

Ser Ser Lys Leu Pro Thr Pro Ser Asn Asn Thr Thr Trp Lys Arg Val
85 90 95
Leu Lys Glu Cys Ala Asp Lys Tyr Ser Tyr Ala Gly Asp Ala Leu Gln
100 105 110
Asp Ser Val Gln Asp Leu Ala Asn Glu Ala Tyr Asp Tyr Ala Tyr Met
115 120 125
His Ile Thr Ala Ala Lys Asp Tyr Pro Asn Ala Cys His Asn Ala Phe
130 135 140
Lys Arg Tyr Pro Gly Leu Val Tyr Pro Arg Asp Leu Ala Arg Arg Glu
145 150 155 160
Asp Gly Leu Lys His Ile Cys Asp Val Ala Met Gly Ile Ile Asp Asn
165 170 175
Leu Asp Trp

<210> 36
<211> 540
<212> DNA
<213> Glycine max

<400> 36
atggtttctt ctaagatctt cttccttttt ctcctctttc tagcacacct tcatcaacat 60
gcatctgttg aaggagattc cagtttgata aagagaactt gcaagaacac caagtactac 120
aatctatgct tctcttcctt caaatctgat ccaagcagtc caaacgcaga tcctaagggc 180
ctagctgtga tcatgattgg aataggaatg accaatgcca cttccacatc ctcctacttg 240
tcttcaaagt tgcctacccc ctccaacaac acaacctgga aaagggtcct caaggagtgt 300
gctgataagt actcctatgc tggatgatgcc ctccaagatt cggtgcagga tttggctaata 360
gaggcttatg actatgctta catgcacatc actgccgcca aagattaccc aaatgcttgc 420
cacaacgctt tcaaacggta ccttggtttg gtttatcctc gtgatcttgc tcgtagagaa 480
gatggtttga agcatatatg cgatgtggca atggggatta tagataatct tgattggtag 540

<210> 37
<211> 766
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (6)...(542)

<400> 37
caaca atg aca aac ttg aag cct cta att ctc tta gcc att att gtt atg 50
Met Thr Asn Leu Lys Pro Leu Ile Leu Leu Ala Ile Ile Val Met
1 5 10 15
att tca ata cca tca agc cac tgc aga acc ttg ctt cca gaa aat gaa 98
Ile Ser Ile Pro Ser Ser His Cys Arg Thr Leu Leu Pro Glu Asn Glu
20 25 30
aag ctg ata gag aac act tgc agg aag acc ccc aac tac aac gtt tgc 146
Lys Leu Ile Glu Asn Thr Cys Arg Lys Thr Pro Asn Tyr Asn Val Cys
35 40 45

ctt gag tct ctg aag gca agc cct ggg agc tcc agt gct gac gtc aca	194
Leu Glu Ser Leu Lys Ala Ser Pro Gly Ser Ser Ser Ala Asp Val Thr	
50 55 60	
ggg cta gct caa atc atg gtg aaa gag atg aag gca aaa gca aac tat	242
Gly Leu Ala Gln Ile Met Val Lys Glu Met Lys Ala Lys Ala Asn Tyr	
65 70 75	
gca ttg aag aga atc cag gag ctg cag agg gtg gga gca ggg cct aat	290
Ala Leu Lys Arg Ile Gln Glu Leu Gln Arg Val Gly Ala Gly Pro Asn	
80 85 90 95	
aag caa aga aga gcc ttg agt tct tgt gtt gat aaa tac aaa acg gtt	338
Lys Gln Arg Arg Ala Leu Ser Ser Cys Val Asp Lys Tyr Lys Thr Val	
100 105 110	
tta att gct gat gtt cca caa gcc act gag gct ctg cag aaa ggg gac	386
Leu Ile Ala Asp Val Pro Gln Ala Thr Glu Ala Leu Gln Lys Gly Asp	
115 120 125	
ccc aag ttt gct gaa gat ggg gct aat gat gct gct aat gag gct acc	434
Pro Lys Phe Ala Glu Asp Gly Ala Asn Asp Ala Ala Asn Glu Ala Thr	
130 135 140	
ttt tgt gag gct gat ttc tct gct ggg aat tcc cca ctc acc aaa cag	482
Phe Cys Glu Ala Asp Phe Ser Ala Gly Asn Ser Pro Leu Thr Lys Gln	
145 150 155	
aac aat gct atg cat gat gtt gct gct gtt act gcc gct att gtt aga	530
Asn Asn Ala Met His Asp Val Ala Ala Val Thr Ala Ala Ile Val Arg	
160 165 170 175	
ttg ttg ctc taa taattctagt tgctgaaacc tatatatatg cttaattgta	582
Leu Leu Leu *	
ttaactaaat atagattata gatgtctctg catcatgctg acttggtgcc tgttaactgt	642
aatgtgaaaa tactatcttt ttataaaaat gttgttatat gtaataaaaat ccaaccctct	702
cgtgattctc acgagtttcc cagaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	762
aaaa	766

<210> 38

<211> 178

<212> PRT

<213> Glycine max

<400> 38

Met Thr Asn Leu Lys Pro Leu Ile Leu Leu Ala Ile Ile Val Met Ile
1 5 10 15
Ser Ile Pro Ser Ser His Cys Arg Thr Leu Leu Pro Glu Asn Glu Lys
20 25 30
Leu Ile Glu Asn Thr Cys Arg Lys Thr Pro Asn Tyr Asn Val Cys Leu
35 40 45

Glu	Ser	Leu	Lys	Ala	Ser	Pro	Gly	Ser	Ser	Ser	Ala	Asp	Val	Thr	Gly
50						55					60				
Leu	Ala	Gln	Ile	Met	Val	Lys	Glu	Met	Lys	Ala	Lys	Ala	Asn	Tyr	Ala
65					70				75					80	
Leu	Lys	Arg	Ile	Gln	Glu	Leu	Gln	Arg	Val	Gly	Ala	Gly	Pro	Asn	Lys
			85					90						95	
Gln	Arg	Arg	Ala	Leu	Ser	Ser	Cys	Val	Asp	Lys	Tyr	Lys	Thr	Val	Leu
			100					105					110		
Ile	Ala	Asp	Val	Pro	Gln	Ala	Thr	Glu	Ala	Leu	Gln	Lys	Gly	Asp	Pro
		115					120					125			
Lys	Phe	Ala	Glu	Asp	Gly	Ala	Asn	Asp	Ala	Ala	Asn	Glu	Ala	Thr	Phe
	130				135						140				
Cys	Glu	Ala	Asp	Phe	Ser	Ala	Gly	Asn	Ser	Pro	Leu	Thr	Lys	Gln	Asn
145					150					155					160
Asn	Ala	Met	His	Asp	Val	Ala	Ala	Val	Thr	Ala	Ala	Ile	Val	Arg	Leu
			165					170						175	
Leu	Leu														

<210> 39
 <211> 537
 <212> DNA
 <213> Glycine max

<400> 39	
atgacaaact tgaagcctct aattctctta gccattattg ttatgatttc aataccatca	60
agccactgca gaaccttgct tccagaaaat gaaaagctga tagagaacac ttgcaggaag	120
acccccaact acaacgtttg ccttgagtct ctgaaggcaa gccctgggag ctccagtgct	180
gacgtcacag ggctagctca aatcatggtg aaagagatga aggcaaaagc aaactatgca	240
ttgaagagaa tccaggagct gcagaggggtg ggagcagggc ctaataagca aagaagagcc	300
ttgagttctt gtgttgataa atacaaaacg gttttaattg ctgatgttcc acaagccact	360
gaggctctgc agaaagggga ccccaagttt gctgaagatg gggctaata tgctgctaata	420
gaggctacct tttgtgaggc tgatttctct gctgggaatt cccactcac caaacagAAC	480
aatgctatgc atgatgttgc tgctgttact gccgctattg ttagattggt gctctaa	537

<210> 40
 <211> 826
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (111)...(719)

<221> misc_feature
 <222> (1)...(826)
 <223> n = A,T,C or G

<400> 40	
aaaagggttag gtccactaca tctgctccta accataaaaaa ggccctagcag cattccattc	60
agtggaaatc agcaactacc aaaaccaatc tctttcaata atcaacaaca atg aca	116
	Met Thr
	1

aac ttg aag cct cta att ctc ttc ttt tat ctc cta gcc att gtt gtt	164
Asn Leu Lys Pro Leu Ile Leu Phe Phe Tyr Leu Leu Ala Ile Val Val	
5 10 15	
atg att tca ata cca tca agc cac tgc agc aga acc ttg ctt cca gaa	212
Met Ile Ser Ile Pro Ser Ser His Cys Ser Arg Thr Leu Leu Pro Glu	
20 25 30	
aac gaa aag ctg ata gag aac act tgc aag aaa act ccc aac tac aac	260
Asn Glu Lys Leu Ile Glu Asn Thr Cys Lys Lys Thr Pro Asn Tyr Asn	
35 40 45 50	
gtt tgc ctt gag tct ctg aag gca agc cct ggg agc tcc agt gct gac	308
Val Cys Leu Glu Ser Leu Lys Ala Ser Pro Gly Ser Ser Ser Ala Asp	
55 60 65	
gtc aca ggg ctg gct caa atc atg gtc aaa gag atg aag gcc aaa gca	356
Val Thr Gly Leu Ala Gln Ile Met Val Lys Glu Met Lys Ala Lys Ala	
70 75 80	
aac gat gca ttg aaa aga atc caa gag ttg cag agg gtg gga gca tcg	404
Asn Asp Ala Leu Lys Arg Ile Gln Glu Leu Gln Arg Val Gly Ala Ser	
85 90 95	
ggg cct aag caa aga aga gcc ttg agt tct tgt gct gat aaa tac aaa	452
Gly Pro Lys Gln Arg Arg Ala Leu Ser Ser Cys Ala Asp Lys Tyr Lys	
100 105 110	
gcg gtt tta att gct gat gtt cca caa gcc act gag gct ctg cag aaa	500
Ala Val Leu Ile Ala Asp Val Pro Gln Ala Thr Glu Ala Leu Gln Lys	
115 120 125 130	
ggt gac ccc aag ttt gct gaa gat ggg gct aat gat gct gct aat gag	548
Gly Asp Pro Lys Phe Ala Glu Asp Gly Ala Asn Asp Ala Ala Asn Glu	
135 140 145	
gct act tat tgt gag act gat ttc tct gca gca ggg aat tcc cca ctc	596
Ala Thr Tyr Cys Glu Thr Asp Phe Ser Ala Ala Gly Asn Ser Pro Leu	
150 155 160	
acc aaa cag aac aat gct atg cat gat gtt gct gct gtt act gcc gct	644
Thr Lys Gln Asn Asn Ala Met His Asp Val Ala Ala Val Thr Ala Ala	
165 170 175	
att gtt aaa ttg ttg ctc caa act ata tat act aaa ttg tac ctg tta	692
Ile Val Lys Leu Leu Leu Gln Thr Ile Tyr Thr Lys Leu Tyr Leu Leu	
180 185 190	
act gta atg gtg aaa ata cta tcc taa ttttaaaagc cttttttata	739
Thr Val Met Val Lys Ile Leu Ser *	
195 200	

aaaatngttt attaatatgt taataaaaat ccaaaccctc cccgtngaat tctcaacaaa 799
 tttcccaaaa aaaaaaaaaa aaaaaaa 826

<210> 41
 <211> 202
 <212> PRT
 <213> Glycine max

<400> 41
 Met Thr Asn Leu Lys Pro Leu Ile Leu Phe Phe Tyr Leu Leu Ala Ile
 1 5 10 15
 Val Val Met Ile Ser Ile Pro Ser Ser His Cys Ser Arg Thr Leu Leu
 20 25 30
 Pro Glu Asn Glu Lys Leu Ile Glu Asn Thr Cys Lys Lys Thr Pro Asn
 35 40 45
 Tyr Asn Val Cys Leu Glu Ser Leu Lys Ala Ser Pro Gly Ser Ser Ser
 50 55 60
 Ala Asp Val Thr Gly Leu Ala Gln Ile Met Val Lys Glu Met Lys Ala
 65 70 75 80
 Lys Ala Asn Asp Ala Leu Lys Arg Ile Gln Glu Leu Gln Arg Val Gly
 85 90 95
 Ala Ser Gly Pro Lys Gln Arg Arg Ala Leu Ser Ser Cys Ala Asp Lys
 100 105 110
 Tyr Lys Ala Val Leu Ile Ala Asp Val Pro Gln Ala Thr Glu Ala Leu
 115 120 125
 Gln Lys Gly Asp Pro Lys Phe Ala Glu Asp Gly Ala Asn Asp Ala Ala
 130 135 140
 Asn Glu Ala Thr Tyr Cys Glu Thr Asp Phe Ser Ala Ala Gly Asn Ser
 145 150 155 160
 Pro Leu Thr Lys Gln Asn Asn Ala Met His Asp Val Ala Ala Val Thr
 165 170 175
 Ala Ala Ile Val Lys Leu Leu Leu Gln Thr Ile Tyr Thr Lys Leu Tyr
 180 185 190
 Leu Leu Thr Val Met Val Lys Ile Leu Ser
 195 200

<210> 42
 <211> 609
 <212> DNA
 <213> Glycine max

<400> 42
 atgacaaaact tgaagcctct aattctcttc ttttatctcc tagccattgt tgttatgatt 60
 tcaataccat caagccactg cagcagaacc ttgcttccag aaaacgaaaa gctgatagag 120
 aacacttgca agaaaactcc caactacaac gtttgcttg agtctctgaa ggcaagccct 180
 gggagctcca gtgctgacgt cacagggctg gctcaaatca tggtaaaga gatgaaggcc 240
 aaagcaaacg atgcattgaa aagaatccaa gagttgcaga gggtagggagc atcggggcct 300
 aagcaaagaa gagccttgag ttcttggtgct gataaatata aagcgggtttt aattgctgat 360
 gttccacaag ccaactgaggc tctgcagaaa ggtgacccca agtttgctga agatggggct 420
 aatgatgctg ctaatgaggc tacttattgt gagactgatt tctctgcagc aggggaattcc 480
 ccactcacca aacagaacaa tgctatgcat gatgttgctg ctgttactgc cgctattggt 540
 aaattgttgc tccaaactat atatactaaa ttgtacctgt taactgtaat ggtgaaaata 600
 ctatcctaa 609

<210> 43
 <211> 983
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (50)...(598)

<400> 43
 ccttcttcat cttctacttc tatctcccta catactcatt caaacagac atg aaa att 58
 Met Lys Ile
 1

atg gaa tca tta gct ctt atc ttc tac agt act ctt gtt tta gct acg 106
 Met Glu Ser Leu Ala Leu Ile Phe Tyr Ser Thr Leu Val Leu Ala Thr
 5 10 15

att tca gtt cca gca act aac tcc aga atc atc cat caa aaa aac aat 154
 Ile Ser Val Pro Ala Thr Asn Ser Arg Ile Ile His Gln Lys Asn Asn
 20 25 30 35

gcc aat ctg att gaa gaa act tgc aag cag aca ccc cat cac gac ctt 202
 Ala Asn Leu Ile Glu Glu Thr Cys Lys Gln Thr Pro His His Asp Leu
 40 45 50

tgc atc caa tac ctg tcc tcc gac cct cgc agc acc gaa gca gat gtg 250
 Cys Ile Gln Tyr Leu Ser Ser Asp Pro Arg Ser Thr Glu Ala Asp Val
 55 60 65

aca ggg ctg gca ctt att atg gtc aac gta atc aaa atc aaa gca aac 298
 Thr Gly Leu Ala Leu Ile Met Val Asn Val Ile Lys Ile Lys Ala Asn
 70 75 80

aat gca ttg gac aaa atc cac caa ctg ctt cag aaa aac cct gaa cct 346
 Asn Ala Leu Asp Lys Ile His Gln Leu Leu Gln Lys Asn Pro Glu Pro
 85 90 95

agt caa aag gaa cca ctg agt tgc tgt gct gct aga tac aaa gca att 394
 Ser Gln Lys Glu Pro Leu Ser Ser Cys Ala Ala Arg Tyr Lys Ala Ile
 100 105 110 115

gtg gaa gct gac gtg gca caa gcc gtt gcg tct ctg cag aaa gga gac 442
 Val Glu Ala Asp Val Ala Gln Ala Val Ala Ser Leu Gln Lys Gly Asp
 120 125 130

ccc aag ttc gca gaa gat ggt gcc aat gat gct gct att gag gcc acc 490
 Pro Lys Phe Ala Glu Asp Gly Ala Asn Asp Ala Ala Ile Glu Ala Thr
 135 140 145

act tgt gag aac agc ttc tct gct ggg aaa tgc cca ctg acc aat cac 538
 Thr Cys Glu Asn Ser Phe Ser Ala Gly Lys Ser Pro Leu Thr Asn His

150	155	160	
aac aat gct atg cac gat gtt gca acc ata act gca gct ata gtt aga			586
Asn Asn Ala Met His Asp Val Ala Thr Ile Thr Ala Ala Ile Val Arg			
165	170	175	

caa ttg ctc tag tgacacttac tccaacggag gggatgatgc aatttaattt	638
Gln Leu Leu *	
180	

tcgtaatatc acattataat tatattttca attaacacaa cataaaatct tgctctcttg	698
ttgggtctctt ctgtaatgga aacacaactg cttttgccac ttcacaattc tcattttctca	758
ctgtcccttc tctctgctt tccacgtttc ttattttcat ttttcttctt tgattcttgg	818
aaaataattg acagcgcacg ggatgtgata tgcctctgtc ttgtgcttct actttcttct	878
aatgtatcat caatttagcc tttttaactt taacaaacat ttgttaatca gatccttcat	938
attatgaaga tattgacatt taaacttaaa aaaaaaaaaa aaaaa	983

<210> 44
 <211> 182
 <212> PRT
 <213> Glycine max

<400> 44	
Met Lys Ile Met Glu Ser Leu Ala Leu Ile Phe Tyr Ser Thr Leu Val	
1 5 10 15	
Leu Ala Thr Ile Ser Val Pro Ala Thr Asn Ser Arg Ile Ile His Gln	
20 25 30	
Lys Asn Asn Ala Asn Leu Ile Glu Thr Cys Lys Gln Thr Pro His	
35 40 45	
His Asp Leu Cys Ile Gln Tyr Leu Ser Ser Asp Pro Arg Ser Thr Glu	
50 55 60	
Ala Asp Val Thr Gly Leu Ala Leu Ile Met Val Asn Val Ile Lys Ile	
65 70 75 80	
Lys Ala Asn Asn Ala Leu Asp Lys Ile His Gln Leu Leu Gln Lys Asn	
85 90 95	
Pro Glu Pro Ser Gln Lys Glu Pro Leu Ser Ser Cys Ala Ala Arg Tyr	
100 105 110	
Lys Ala Ile Val Glu Ala Asp Val Ala Gln Ala Val Ala Ser Leu Gln	
115 120 125	
Lys Gly Asp Pro Lys Phe Ala Glu Asp Gly Ala Asn Asp Ala Ala Ile	
130 135 140	
Glu Ala Thr Thr Cys Glu Asn Ser Phe Ser Ala Gly Lys Ser Pro Leu	
145 150 155 160	
Thr Asn His Asn Asn Ala Met His Asp Val Ala Thr Ile Thr Ala Ala	
165 170 175	
Ile Val Arg Gln Leu Leu	
180	

<210> 45
 <211> 549
 <212> DNA
 <213> Glycine max

<400> 45
atgaaaatta tggaatcatt agctcttata ttctacagta ctcttgTTTT agctacgatt 60
tcagttccag caactaactc cagaatcatt catcaaaaa acaatgccaa tctgattgaa 120
gaaacttgca agcagacacc ccatcacgac ctttgcatcc aatacctctc ctccgaccct 180
cgcagcaccg aagcagatgt gacagggctg gcacttatta tggccaacgt aatcaaaatc 240
aaagcaaaca atgcattgga caaaatccac caactgcttc agaaaaaacc tgaacctagt 300
caaaaggaac cactgagttc gtgtgctgct agatacaaag caattgtgga agctgacgtg 360
gcacaagccg ttgcgtctct gcagaaagga gaccccaagt tcgcagaaga tggtgccaat 420
gatgctgcta ttgaggccac cacttgtgag aacagcttct ctgctgggaa atcgccactc 480
accaatcaca acaatgctat gcacgatgtt gcaaccataa ctgcagctat agttagacaa 540
ttgctctag 549

<210> 46
<211> 609
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (16) ... (609)

<400> 46
gtttatacca aataa atg atg tta caa gct tct ttt ttg cgc ttg atc tct 51
Met Met Leu Gln Ala Ser Phe Leu Arg Leu Ile Ser
1 5 10

ttc ttc ttt ctc atc gca ctc cct ctt gga aga agc tct acc acc ttg 99
Phe Phe Phe Leu Ile Ala Leu Pro Leu Gly Arg Ser Ser Thr Thr Leu
15 20 25

aat gta cca aag gac ata atc aac caa aca tgc caa aaa tgt gcc aac 147
Asn Val Pro Lys Asp Ile Ile Asn Gln Thr Cys Gln Lys Cys Ala Asn
30 35 40

caa tcc atc atc ttg agc tac aag cta tgc tcc act tct ctt ccg acg 195
Gln Ser Ile Ile Leu Ser Tyr Lys Leu Cys Ser Thr Ser Leu Pro Thr
45 50 55 60

gtt ccg gtg agt cac tcc gca aat ctc gaa ggg ttg gcg ttg gtt gca 243
Val Pro Val Ser His Ser Ala Asn Leu Glu Gly Leu Ala Leu Val Ala
65 70 75

atg gag cta gca cta gag aat gtc act agc act ttg gca atc ata gag 291
Met Glu Leu Ala Leu Glu Asn Val Thr Ser Thr Leu Ala Ile Ile Glu
80 85 90

aag cta tta gat agc aca agt ttg gat aat tct gct ttg ggg tgc tta 339
Lys Leu Leu Asp Ser Thr Ser Leu Asp Asn Ser Ala Leu Gly Cys Leu
95 100 105

gca gat tgc ttg gaa ctg tac tct gat gca gca tgg aca ata ctg aat 387
Ala Asp Cys Leu Glu Leu Tyr Ser Asp Ala Ala Trp Thr Ile Leu Asn
110 115 120

tcc gta ggt gtt ttc ttg tct ggg aat tat gat gta act agg att tgg 435
Ser Val Gly Val Phe Leu Ser Gly Asn Tyr Asp Val Thr Arg Ile Trp
125 130 135 140

gag aga ggt gaa gct tct cct ttg aca cag gag aat tat aat ctc ttt 531
Glu Arg Gly Glu Ala Ser Pro Leu Thr Gln Glu Asn Tyr Asn Leu Phe
160 165 170

gta cct tat tct caa tta ttc cac aga taa 609
Val Pro Tyr Ser Gln Leu Phe His Arg *
190 195

[illegible]

<210> 48
 <211> 594
 <212> DNA
 <213> Glycine max

<400> 48
 atgatgttac aagcttcttt tttgcgcttg atctctttct tctttctcat cgcactccct 60
 cttggaagaa gctctaccac cttgaatgta ccaaaggaca taatcaacca aacatgccaa 120
 aaatgtgcca accaatccat catcttgagc tacaagctat gctccacttc tcttccgacg 180
 gttccgggtga gtcactccgc aaatctcgaa ggggtggcgt tgggtgcaat ggagctagca 240
 ctagagaatg tcactagcac tttggcaatc atagagaagc tattagatag cacaagtttg 300
 gataattctg ctttgggggtg cttagcagat tgcttggaaac tgtactctga tgcagcatgg 360
 acaatactga attccgtagg tgttttcttg tctgggaatt atgatgtaac taggatttgg 420
 atgagttcag ttatggaagc agcatcaaca tgccaacaag gttttactga gagaggtgaa 480
 gcttctcctt tgacacagga gaattataat ctctttcagt tgtgtggtat tgcactttgc 540
 attattcatt tgggtacacc tggagtacct tattctcaat tattccacag ataa 594

<210> 49
 <211> 673
 <212> DNA
 <213> Triticum l

<220>
 <221> CDS
 <222> (33)...(551)

<400> 49
 cagaaacaca agaaaatcgt tgtagcaaag cc atg agg cca tca caa gct ctc 53
 Met Arg Pro Ser Gln Ala Leu
 1 5

tcg ctt ctc gtt gtt gtc ctc ctc ctc gtc tgc tcc agt gct tcc atc 101
 Ser Leu Leu Val Val Val Leu Leu Leu Val Ser Ser Ser Ala Ser Ile
 10 15 20

cta gaa gat acc tgc aag cgc ttc gac ggc gct gac atc tat gat atc 149
 Leu Glu Asp Thr Cys Lys Arg Phe Asp Gly Ala Asp Ile Tyr Asp Ile
 25 30 35

tgc atc aag ttc ttc aag gcc aac aag gac agc gcc acc aca gac aag 197
 Cys Ile Lys Phe Phe Lys Ala Asn Lys Asp Ser Ala Thr Thr Asp Lys
 40 45 50 55

cgt ggc ctt gct gtc att gcc act aag att gcc agt gcg aca gct gtg 245
 Arg Gly Leu Ala Val Ile Ala Thr Lys Ile Ala Ser Ala Thr Ala Val
 60 65 70

gac acc cgc aag cgc att gcc atc ctg aag gcc gag gaa aag gac cat 293
 Asp Thr Arg Lys Arg Ile Ala Ile Leu Lys Ala Glu Glu Lys Asp His
 75 80 85

atg atc caa cag gtc ctc gcc tac tgt gac aat atg tac tcc aga gct 341
Met Ile Gln Gln Val Leu Ala Tyr Cys Asp Asn Met Tyr Ser Arg Ala
90 95 100

atg ggc ttg ttt gac aaa gct gcc agg ggc atc ttg tca ggc agg ttg 389
Met Gly Leu Phe Asp Lys Ala Ala Arg Gly Ile Leu Ser Gly Arg Leu
105 110 115

ggc gac gcg gtg acg agc ctc agc tcc gcg ttg gat att ccc aaa tat 437
Gly Asp Ala Val Thr Ser Leu Ser Ser Ala Leu Asp Ile Pro Lys Tyr
120 125 130 135

tgc gat gac gag ttc ctc gag gca ggc gtg aag tca ccg ttc gat gcc 485
Cys Asp Asp Glu Phe Leu Glu Ala Gly Val Lys Ser Pro Phe Asp Ala
140 145 150

gag aac agc gag ttc gag atg caa tgt gcc ata act ctg ggt gta acg 533
Glu Asn Ser Glu Phe Glu Met Gln Cys Ala Ile Thr Leu Gly Val Thr
155 160 165

aag atg ctg acc ttc tag ttagctagcc agcgaggata tgaatctagg 581
Lys Met Leu Thr Phe *
170

taactacaac aagattccat agtaattttg atgagcaaac tcctcaaaat taataagccc 641
acaatgttat cactgaaaaa aaaaaaaaaa aa 673

<210> 50
<211> 172
<212> PRT
<213> Triticum 1

<400> 50
Met Arg Pro Ser Gln Ala Leu Ser Leu Leu Val Val Val Leu Leu Leu
1 5 10 15
Val Ser Ser Ser Ala Ser Ile Leu Glu Asp Thr Cys Lys Arg Phe Asp
20 25 30
Gly Ala Asp Ile Tyr Asp Ile Cys Ile Lys Phe Phe Lys Ala Asn Lys
35 40 45
Asp Ser Ala Thr Thr Asp Lys Arg Gly Leu Ala Val Ile Ala Thr Lys
50 55 60
Ile Ala Ser Ala Thr Ala Val Asp Thr Arg Lys Arg Ile Ala Ile Leu
65 70 75 80
Lys Ala Glu Glu Lys Asp His Met Ile Gln Gln Val Leu Ala Tyr Cys
85 90 95
Asp Asn Met Tyr Ser Arg Ala Met Gly Leu Phe Asp Lys Ala Ala Arg
100 105 110
Gly Ile Leu Ser Gly Arg Leu Gly Asp Ala Val Thr Ser Leu Ser Ser
115 120 125
Ala Leu Asp Ile Pro Lys Tyr Cys Asp Asp Glu Phe Leu Glu Ala Gly
130 135 140
Val Lys Ser Pro Phe Asp Ala Glu Asn Ser Glu Phe Glu Met Gln Cys
145 150 155 160

Ala Ile Thr Leu Gly Val Thr Lys Met Leu Thr Phe
165 170

<210> 51
<211> 519
<212> DNA
<213> Triticum 1

<400> 51
atgaggccat cacaagctct ctgcttctc gttgttgtcc tcctcctcgt ctcgctccagt 60
gcttccatcc tagaagatac ctgcaagcgc ttcgacggcg ctgacatcta tgatatctgc 120
atcaagttct tcaaggccaa caaggacagc gccaccacag acaagcgtgg ccttgctgtc 180
attgccacta agattgccag tgcgacagct gtggacaccc gcaagcgcgt tgccatcctg 240
aaggccgagg aaaaggacca tatgatccaa caggctcctcg cctactgtga caatatgtac 300
tccagagcta tgggcttgtt tgacaaagct gccaggggca tcttgtcagg caggttgggc 360
gacgcggtga cgagcctcag ctccgcgttg gatattccca aatattgcga tgacgagttc 420
ctcgaggcag gcgtgaagtc accgttcgat gccgagaaca gcgagttcga gatgcaatgt 480
gccataactc tgggtgtaac gaagatgctg accttctag 519

<210> 52
<211> 665
<212> DNA
<213> Triticum 1.

<220>
<221> CDS
<222> (33)...(551)

<400> 52
cagaaacaca agaaaattgt tgcggcaaaa cc atg agg tcg ccg caa gct ctc 53
Met Arg Ser Pro Gln Ala Leu
1 5

tcg ctt ctt gtt gtt gtc ctc ctc ctt gcc tcg tcc agt gct tcc gtc 101
Ser Leu Leu Val Val Val Leu Leu Leu Ala Ser Ser Ser Ala Ser Val
10 15 20

ata gaa gac aca tgc agg cgc ttc gat ggt gct gac atc tac gat atc 149
Ile Glu Asp Thr Cys Arg Arg Phe Asp Gly Ala Asp Ile Tyr Asp Ile
25 30 35

tgc atc aag ttc ttc aag gcc aac aag gat agc gcc acc acg gac aag 197
Cys Ile Lys Phe Phe Lys Ala Asn Lys Asp Ser Ala Thr Thr Asp Lys
40 45 50 55

cgt gcc ctt gct gtc atc gcc att ggg att gcc agt gcg aca gct gtg 245
Arg Gly Leu Ala Val Ile Ala Ile Gly Ile Ala Ser Ala Thr Ala Val
60 65 70

gac acc cgc aag cgc gtc gcc acc ctg aag gcc gag gaa aag gat caa 293
Asp Thr Arg Lys Arg Val Ala Thr Leu Lys Ala Glu Glu Lys Asp Gln
75 80 85

att atc cag cat gtc ctc gcc tac tgt gac aat atg tac tcc agt gtt 341
 Ile Ile Gln His Val Leu Ala Tyr Cys Asp Asn Met Tyr Ser Ser Val
 90 95 100

gtg ggc cta ttt gac aag gct gcc agg ggc atc tcg ttg ggc agg ttg 389
 Val Gly Leu Phe Asp Lys Ala Ala Arg Gly Ile Ser Leu Gly Arg Leu
 105 110 115

ggc gac gca gtg acg agc ctc agc tcc gca ctg gac att ccc aaa tat 437
 Gly Asp Ala Val Thr Ser Leu Ser Ser Ala Leu Asp Ile Pro Lys Tyr
 120 125 130 135

tgc gat gac aag ttc ctc gag gca ggc gtg aag tcg cca ttc gat gcc 485
 Cys Asp Asp Lys Phe Leu Glu Ala Gly Val Lys Ser Pro Phe Asp Ala
 140 145 150

gag aac agc gag ttc gag gtg caa tgt gca atc act ctg ggt gta acg 533
 Glu Asn Ser Glu Phe Glu Val Gln Cys Ala Ile Thr Leu Gly Val Thr
 155 160 165

aag atg ctg acc atg tag ttagcgagtc ggcgaggaca tgaatgtggg 581
 Lys Met Leu Thr Met *
 170

aaactacaat aagagtccat agtaatttcg atgagtaaac tcctcaaat taataagccc 641
 aaaaaaaaaa aaaaaaaaaa aaaa 665

<210> 53
 <211> 172
 <212> PRT
 <213> Triticum l.

<400> 53
 Met Arg Ser Pro Gln Ala Leu Ser Leu Leu Val Val Val Leu Leu Leu
 1 5 10 15
 Ala Ser Ser Ser Ala Ser Val Ile Glu Asp Thr Cys Arg Arg Phe Asp
 20 25 30
 Gly Ala Asp Ile Tyr Asp Ile Cys Ile Lys Phe Phe Lys Ala Asn Lys
 35 40 45
 Asp Ser Ala Thr Thr Asp Lys Arg Gly Leu Ala Val Ile Ala Ile Gly
 50 55 60
 Ile Ala Ser Ala Thr Ala Val Asp Thr Arg Lys Arg Val Ala Thr Leu
 65 70 75 80
 Lys Ala Glu Glu Lys Asp Gln Ile Ile Gln His Val Leu Ala Tyr Cys
 85 90 95
 Asp Asn Met Tyr Ser Ser Val Val Gly Leu Phe Asp Lys Ala Ala Arg
 100 105 110
 Gly Ile Ser Leu Gly Arg Leu Gly Asp Ala Val Thr Ser Leu Ser Ser
 115 120 125
 Ala Leu Asp Ile Pro Lys Tyr Cys Asp Asp Lys Phe Leu Glu Ala Gly
 130 135 140
 Val Lys Ser Pro Phe Asp Ala Glu Asn Ser Glu Phe Glu Val Gln Cys
 145 150 155 160

Ala Ile Thr Leu Gly Val Thr Lys Met Leu Thr Met
 165 170

<210> 54
 <211> 519
 <212> DNA
 <213> Triticum l

<400> 54
 atgaggtcgc cgcaagctct ctcgcttctt gttgttgtec tcttccttgc ctcgctccagt 60
 gcttccgtca tagaagacac atgcaggcgc ttcgatggtg ctgacatcta cgatatctgc 120
 atcaagttct tcaaggccaa caaggatagc gccaccacgg acaagcgtgg ccttgctgtc 180
 atcgccattg ggattgccag tgcgacagct gtggacaccc gcaagcgcgt cgccaccctg 240
 aaggccgagg aaaaggatca aattatccag catgtcctcg cctactgtga caatatgtac 300
 tccagtgttg tgggcctatt tgacaaggct gccaggggca tctcgttggg caggttgggc 360
 gacgcagtga cgagcctcag ctccgcactg gacattccca aatattgcga tgacaagttc 420
 ctcgaggcag gcgtgaagtc gccattcgat gccgagaaca gcgagttcga ggtgcaatgt 480
 gcaatcactc tgggtgtaac gaagatgctg accatgtag 519